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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:29:28 ; Search time 53 Seconds
(without alignments)
613.075 Million cell updates/sec

Title: US-09-620-955b-2

Perfect score: 115

Sequence: 1 QVQLQESGGGLVQPGSLRL.....CARDYFDLWGRGIVTVSS 115

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 934974

Minimum DB seq length: 0

Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database : A: Genesep29Jan04:*

- 1: Genesep1980s:*
- 2: Genesep1990s:*
- 3: Genesep2000s:*
- 4: Genesep2001s:*
- 5: Genesep2002s:*
- 6: Genesep2003as:*
- 7: Genesep2003bs:*
- 8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	115	100.0	115	4	AAB69601 Huntingti
2	65	56.5	115	5	AAM51164 Anti-tumo
3	63	54.8	98	3	AAB40116 Anti-hill
4	63	54.8	98	3	AAB40104 Anti-hill
5	63	54.8	98	3	AAB40118 Anti-hill
6	63	54.8	98	3	AAB40115 Anti-hill
7	63	54.8	98	3	AAB40120 Anti-hill
8	63	54.8	98	3	AAB40105 Anti-hill
9	63	54.8	98	3	AAB40106 Anti-hill
10	63	54.8	98	3	AAB40102 Anti-hill
11	63	54.8	98	3	AAB40101 Anti-hill
12	63	54.8	98	3	AAB40110 Anti-hill
13	63	54.8	98	3	AAB40117 Anti-hill
14	63	54.8	98	3	AAB40128 Anti-hill
15	63	54.8	98	3	AAB40099 Anti-hill
16	63	54.8	98	4	AAB67512 Heavy cha
17	63	54.8	98	4	AAB67507 Light cha
18	63	54.8	98	4	ABG78201 Human Fv
19	63	54.8	98	5	ABG78199 Human Fv
20	63	54.8	98	5	ABG78200 Human Fv
21	63	54.8	98	5	ABG78200 Human Fv
22	63	54.8	98	5	ABG91890 Human ant
23	63	54.8	98	5	ABG91891 Human ant
24	63	54.8	98	5	ABG91892 Human ant
25	63	54.8	98	6	ABO27091 Human ger

26	63	54.8	98	7	ADC99832 Germline
27	63	54.8	98	7	ADC99833 Anti-huma
28	63	54.8	98	7	ADD05436 Anti-MUC1
29	63	54.8	98	7	ADD05437 Anti-MUC1
30	63	54.8	113	4	AAU02538 Anti-adip
31	63	54.8	113	4	AAU02537 Anti-adip
32	62	53.9	98	3	AAU02537 Anti-adip
33	62	53.9	98	3	AAU02537 Anti-adip
34	62	53.9	98	3	AAU02537 Anti-adip
35	62	53.9	98	3	AAU02537 Anti-adip
36	62	53.9	98	5	ABG78205 Human Fv
37	62	53.9	98	5	ABG78205 Human Fv
38	62	53.9	98	5	ABG78205 Human Fv
39	62	53.9	98	5	ABG78205 Human Fv
40	62	53.9	98	6	ABO27092 Human ger
41	62	53.9	98	6	ABO27092 Human ger
42	62	53.9	98	6	ABO27092 Human ger
43	62	53.9	98	6	ABO27092 Human ger
44	62	53.9	98	6	ABO27092 Human ger
45	62	53.9	98	6	ABO27092 Human ger
46	62	53.9	98	6	ABO27092 Human ger
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49	62	53.9	98	6	ABO27092 Human ger
50	62	53.9	98	6	ABO27092 Human ger
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53	62	53.9	98	6	ABO27092 Human ger
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59	62	53.9	98	6	ABO27092 Human ger
60	62	53.9	98	6	ABO27092 Human ger
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62	62	53.9	98	6	ABO27092 Human ger
63	62	53.9	98	6	ABO27092 Human ger
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66	62	53.9	98	6	ABO27092 Human ger
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71	62	53.9	98	6	ABO27092 Human ger
72	62	53.9	98	6	ABO27092 Human ger
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77	62	53.9	98	6	ABO27092 Human ger
78	62	53.9	98	6	ABO27092 Human ger
79	62	53.9	98	6	ABO27092 Human ger
80	62	53.9	98	6	ABO27092 Human ger
81	62	53.9	98	6	ABO27092 Human ger
82	62	53.9	98	6	ABO27092 Human ger
83	62	53.9	98	6	ABO27092 Human ger
84	62	53.9	98	6	ABO27092 Human ger
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88	62	53.9	98	6	ABO27092 Human ger
89	62	53.9	98	6	ABO27092 Human ger
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95	62	53.9	98	6	ABO27092 Human ger
96	62	53.9	98	6	ABO27092 Human ger
97	62	53.9	98	6	ABO27092 Human ger
98	62	53.9	98	6	ABO27092 Human ger

99 39 33.9 109 7 ADC60990 Human ant
100 39 33.9 112 2 AAR12274 Anti-huma

ALIGNMENTS

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RESULT 1
AAB69601
ID AAB69601 standard; protein; 115 AA.
AC AAB69601;
XX
DT 30-APR-2001 (first entry)
XX
DE Huntingtin minimal svf binding region #1.
XX
KW Neurological disorder; Huntington's disease; Alzheimer's disease;
KW Parkinson's disease; prion disease; frontotemporal dementia;
KW amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy;
KW dentatorubal-pallidoluyisan atrophy; spinocerebellar ataxia type 1, SCA2;
KW SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody.
XX
OS Unidentified.
XX
PN WO200106989-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020131.
XX
PR 27-JUL-1999; 99US-0146047P.
PR 21-JUL-2000; 2000US-00620955.
XX
PA (HUST/) HUSTON J S.
PA (MESS/) MESSER A.
PA (LECE/) LECERF J.
XX
PI Huston JS, Messer A, Lecerf J;
XX
WPI; 2001-192700/19.
DR N-PSDB; AAF58705.
XX
PT Inhibiting intracellular polypeptide accumulation, useful for treating
PT neurological disorders, e.g. Alzheimer's disease, comprises contacting
PT the polypeptide with a specific intrabody.
XX
PS Claim 21; Page 93; 108pp; English.
XX
The present invention describes a method for inhibiting the formation of
aggregates of certain proteins, involving contacting the protein with a
binding molecule known as an intrabody. Proteins to be bound include
those associated with neurological disorders, and so the method can be
used in the prevention of diseases such as Alzheimer's, Parkinson's and
Huntington's diseases, prion disease, frontotemporal dementia,
amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy,
dentatorubal-pallidoluyisan atrophy, spinocerebellar ataxia type 1
(SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7
XX
SQ Sequence 115 AA;
Query Match 100.0%; Score 115; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.9e-104;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVQLQESGGGLVPGGSLRLSCAASGFTFSYSMSWVRQAPGKLEWVAIVSDGSKYY 60
Db 1 QVQLQESGGGLVPGGSLRLSCAASGFTFSYSMSWVRQAPGKLEWVAIVSDGSKYY 60
Qy 61 ADSVKGRFTTSDNSKNTLYLQMSLRAEDTAVYYCARDRYFDLWGRGLTVTSS 115
Db 61 ADSVKGRFTTSDNSKNTLYLQMSLRAEDTAVYYCARDRYFDLWGRGLTVTSS 115

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RESULT 2
AAM51164
ID AAM51164 standard; protein; 115 AA.
XX
AC AAM51164;
XX
DT 10-JUN-2002 (first entry)
XX
DE Anti-tumour necrosis factor antibody heavy chain variable region.
XX
KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW complementarity determining region; antirheumatic; antithratic;
KW antiulcer; antiasthmatic; anti allergic; antinflammatory; antisticking;
KW antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;
KW antiangular; cardiac; antibacterial; virucide; fungicide; antileptotic;
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PH Key
FT Region Location/Qualifiers
FT 1..30 /label= FR1
FT 31..35 /label= CDR1
FT 36..49 /label= FR2
FT 50..66 /label= CDR2
FT 67..98 /label= FR3
FT 99..107 /label= CDR3
FT 108..115 /label= J6
XX
WO200212502-A2.
XX
14-FEB-2002.
XX
07-AUG-2001; 2001WO-US024785.
XX
07-AUG-2000; 2000US-0223360P.
XX
29-SEP-2000; 2000US-0236826P.
XX
01-AUG-2001; 2001US-00920137.
XX
(CENZ ) CENTOCOR INC.
XX
Giles-Komar J, Knight DM, Heavner G, Scallan B, Shealy D;
XX
WPI; 2002-217194/27.
XX
Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
angina pectoris, myocardial infarction, leprosy.
XX
Claim 9; Page 129; 131pp; English.
XX
The present sequence is that of the heavy chain variable region of an
anti-tumour necrosis factor (TNF) antibody of the invention. The
invention provides isolated human, primate, rodent, mammalian, chimeric,
humanised and/or complementarity determining region (CDR)-grafted anti-
TNF antibodies, immunoglobulins, cleavage products and other specified
portions and variants, as well as anti-TNF antibody compositions,
encoding or complementary nucleic acids, vectors, host cells,
compositions, formulations, devices, transgenic animals, transgenic
plants, and methods of making and using them. The anti-TNF antibody
comprises at least a portion of an immunoglobulin molecule, especially
the heavy chain and/or light chain variable regions given in the present
sequence and in AAM51165, or either all of the CDRs of the heavy chain
(see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
63). The antibody may inhibit TNF-induced cell adhesion molecules,

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CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
 CC in a mouse model. It is useful for diagnosing or treating a TNF related
 CC condition in a cell, tissue, organ or animal (claimed) such as rheumatoid
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
 CC sickle cell anemia, diabetes, a cardiovascular disease such as
 CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
 CC myocardial infarction, an infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy and malaria a malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
 CC Creutzfeldt-Jakob disease
 CC
 SQ Sequence 115 AA;
 Query Match 56.5%; Score 65; DB 5; Length 115;
 Best Local Similarity 100.0%; Pred. No. 3.1e-55;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
 DB 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
 QY 96 CARDR 100
 DB 96 CARDR 100
 RESULT 3
 AAB40116
 ID AAB40116 standard; protein; 98 AA.
 AC AAB40116;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 642.
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 XX (GENY) GENETICS INST INC.
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.
 DR
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Claim 75; Page 122; 377pp; English.
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human

CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40058-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiasthmatic; antiparasitic;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 SQ Sequence 98 AA;
 Query Match 54.8%; Score 63; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
 DB 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
 QY 96 CAR 98
 DB 96 CAR 98
 RESULT 4
 AAB40104
 ID AAB40104 standard; protein; 98 AA.
 XX
 AC AAB40104;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 630.
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 XX (GENY) GENETICS INST INC.
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.
 DR
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX

PS Claim 75; Page 121; 377pp; English.

XX This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences AAB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region amino acid sequences. Other variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771 represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063 represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and construction of the antibodies of the invention are given in AAC61062-C61071. The antibody of the invention is a neutralising antibody and has antirheumatic; antiarthritic; antisclerotic; antiinflammatory; antineuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antigen binding fragments are useful in the treatment of disorders associated with detrimental release of human IL-12, especially Crohn's disease, multiple sclerosis and rheumatoid arthritis. They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12 disorders

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95
|||
36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95

Db 96 CAR 98
|||
96 CAR 98

RESULT 5
AAB40118
ID AAB40118 standard; protein; 98 AA.
AC AAB40118;
XX
XX 05-FEB-2001 (first entry)
XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 644.
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX Homo sapiens.
XX WO200056772-A1.
XX 28-SEP-2000.
XX 24-MAR-2000; 2000WO-US007946.
XX 25-MAR-1999; 99US-0126603P.
XX (BADI) BASF AG.
XX (GEMY) GENETICS INST INC.
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Wyles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX Derbyshire EJ, Carmen S, Smith S, Hollett TL, Du Fou SL;
XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohn's disease and multiple sclerosis.

XX Claim 75; Page 122; 377pp; English.

XX This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences AAB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region amino acid sequences. Other variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771 represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063 represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and construction of the antibodies of the invention are given in AAC61062-C61071. The antibody of the invention is a neutralising antibody and has antirheumatic; antiarthritic; antisclerotic; antiinflammatory; antineuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antigen binding fragments are useful in the treatment of disorders associated with detrimental release of human IL-12, especially Crohn's disease, multiple sclerosis and rheumatoid arthritis. They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12 disorders

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95
|||
36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95

Db 96 CAR 98
|||
96 CAR 98

RESULT 6
AAB40115
ID AAB40115 standard; protein; 98 AA.
AC AAB40115;
XX
XX 05-FEB-2001 (first entry)
XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 641.
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX Homo sapiens.
XX WO200056772-A1.
XX 28-SEP-2000.
XX 24-MAR-2000; 2000WO-US007946.
XX 25-MAR-1999; 99US-0126603P.
XX (BADI) BASF AG.
XX (GEMY) GENETICS INST INC.
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;

PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX WPI; 2000-638250/61.
XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis.
XX Claim 75; Page 122; 377pp; English.
XX This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in AAC61062-
CC C61071. The antibody of the invention is a neutralising antibody and has
CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
CC antibacterial and immunosuppressive activity. The antibodies or antigen-
CC binding fragments are useful in the treatment of disorders associated
CC with detrimental release of human IL-12, especially Crohn's disease,
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
CC manufacture of a pharmaceutical composition to treat human IL-12
CC disorders
XX
SQ Sequence 98 AA;
Query Match 54.8%; Score 63; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98
RESULT 7
AAB40120
ID AAB40120 standard; protein; 98 AA.
AC AAB40120;
XX
XX 05-FEB-2001 (first entry)
XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 646.
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritic;
XX antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX Homo sapiens.
XX WO2000056772-A1.
XX 28-SEP-2000.
XX 24-MAR-2000; 2000WO-US007946.
XX 25-MAR-1999; 99US-0126603P.

XX (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX WPI; 2000-638250/61.
XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis.
XX Claim 75; Page 122; 377pp; English.
XX This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in AAC61062-
CC C61071. The antibody of the invention is a neutralising antibody and has
CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
CC antibacterial and immunosuppressive activity. The antibodies or antigen-
CC binding fragments are useful in the treatment of disorders associated
CC with detrimental release of human IL-12, especially Crohn's disease,
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
CC manufacture of a pharmaceutical composition to treat human IL-12
CC disorders
XX
SQ Sequence 98 AA;
Query Match 54.8%; Score 63; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98
RESULT 8
AAB40105
ID AAB40105 standard; protein; 98 AA.
XX
XX AAB40105;
XX
XX 05-FEB-2001 (first entry)
XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 631.
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritic;
XX antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX Homo sapiens.
XX WO2000056772-A1.
XX

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PD 28-SEP-2000.
XX
XX
XX PF 24-MAR-2000; 2000WO-US007945.
XX
XX PR 25-MAR-1999; 99US-0126603P.
XX
XX PA (BADI ) BASF AG.
XX (GEMY ) GENETICS INST INC.
XX
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
XX PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
XX WPI; 2000-638250/61.
XX
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XX PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX PT disease and multiple sclerosis.
XX
XX PS Claim 75; Page 121; 377pp; English.
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XX CC interleukin-12 (IL-12). The invention also includes antigen binding
XX CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX CC anti-IL-12 antibody heavy and light chain complementarity determining
XX CC region (CDR) amino acid sequences, and also includes variable region
XX CC amino acid sequences. Other variable region amino acid sequences are
XX CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX CC represent other CDR sequences. Light chain CDR3 consensus sequences are
XX CC given in AAB40064-B40067. Primers used in the identification and
XX CC construction of the antibodies of the invention are given in AAC61062-
XX CC C61071. The antibody of the invention is a neutralising antibody and has
XX CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
XX CC neuroprotective; antipaprositic; antiasthmatic; cardiant; antiparasitic;
XX CC antibacterial and immunosuppressive activity. The antibodies or antigen-
XX CC binding fragments are useful in the treatment of disorders associated
XX CC with detrimental release of human IL-12, especially Crohn's disease,
XX CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
XX CC manufacture of a pharmaceutical composition to treat human IL-12
XX CC disorders
XX
XX SQ Sequence 98 AA;
XX
XX Query Match 54.8%; Score 63; DB 3; Length 98;
XX Best Local Similarity 100.0%; Pred. NO. 2.4e-53;
XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVVY 95
XX |||||
XX DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVVY 95
XX |||||
XX QY 96 CAR 98
XX |||||
XX DB 96 CAR 98
XX |||||
XX
XX RESULT 9
XX AAB40106
XX ID AAB40106 standard; protein; 98 AA.
XX
XX AC AAB40106;
XX
XX XX 05-FEB-2001 (first entry)
XX
XX DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 632.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX KW complementarity determining region; CDR; antirheumatic; antiarthritic;
XX KW antisclerotic; neuroprotective; antipaprositic; antiasthmatic; cardiant;
XX KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX KW multiple sclerosis; rheumatoid arthritis.

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XX OS Homo sapiens.
XX
XX PN WO200056772-A1.
XX
XX PD 28-SEP-2000.
XX
XX PF 24-MAR-2000; 2000WO-US007945.
XX
XX PR 25-MAR-1999; 99US-0126603P.
XX
XX PA (BADI ) BASF AG.
XX (GEMY ) GENETICS INST INC.
XX
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
XX PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
XX PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
XX WPI; 2000-638250/61.
XX
XX New human antibody specific for human interleukin-12 (IL-12) used to
XX PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX PT disease and multiple sclerosis.
XX
XX PS Claim 75; Page 121; 377pp; English.
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XX CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX CC anti-IL-12 antibody heavy and light chain complementarity determining
XX CC region (CDR) amino acid sequences, and also includes variable region
XX CC amino acid sequences. Other variable region amino acid sequences are
XX CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX CC represent other CDR sequences. Light chain CDR3 consensus sequences are
XX CC given in AAB40064-B40067. Primers used in the identification and
XX CC construction of the antibodies of the invention are given in AAC61062-
XX CC C61071. The antibody of the invention is a neutralising antibody and has
XX CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
XX CC neuroprotective; antipaprositic; antiasthmatic; cardiant; antiparasitic;
XX CC antibacterial and immunosuppressive activity. The antibodies or antigen-
XX CC binding fragments are useful in the treatment of disorders associated
XX CC with detrimental release of human IL-12, especially Crohn's disease,
XX CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
XX CC manufacture of a pharmaceutical composition to treat human IL-12
XX CC disorders
XX
XX SQ Sequence 98 AA;
XX
XX Query Match 54.8%; Score 63; DB 3; Length 98;
XX Best Local Similarity 100.0%; Pred. NO. 2.4e-53;
XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVVY 95
XX |||||
XX DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVVY 95
XX |||||
XX QY 96 CAR 98
XX |||||
XX DB 96 CAR 98
XX |||||
XX
XX RESULT 10
XX AAB40102
XX ID AAB40102 standard; protein; 98 AA.
XX
XX AC AAB40102;
XX
XX XX 05-FEB-2001 (first entry)
XX
XX DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 628.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX KW complementarity determining region; CDR; antirheumatic; antiarthritic;
XX KW antisclerotic; neuroprotective; antipaprositic; antiasthmatic; cardiant;
XX KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX KW multiple sclerosis; rheumatoid arthritis.

```

KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX Homo sapiens.
 XX WO200056772-A1.
 XX 28-SEP-2000.
 XX 24-MAR-2000; 2000WO-US007946.
 XX 25-MAR-1999; 99US-0126603P.
 XX (BADI) BASF AG.
 XX (GEMY) GENETICS INST INC.
 XX Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M;
 XX Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 XX Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 XX Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 XX disease and multiple sclerosis.
 XX Claim 75; Page 121; 377pp; English.
 XX This invention relates to a new human antibody specific for human
 XX interleukin-12 (IL-12). The invention also includes antigen binding
 XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 XX anti-IL-12 antibody heavy and light chain complementarity determining
 XX region (CDR) amino acid sequences, and also includes variable region
 XX amino acid sequences. Other variable region amino acid sequences are
 XX given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 XX represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 XX represent other CDR sequences. Light chain CDR3 consensus sequences are
 XX given in AAB40064-B40067. Primers used in the identification and
 XX construction of the antibodies of the invention are given in AAC61062-
 XX C61071. The antibody of the invention is a neutralising antibody and has
 XX antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 XX neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 XX antibacterial and immunosuppressive activity. The antibodies or antigen-
 XX binding fragments are useful in the treatment of disorders associated
 XX with detrimental release of human IL-12, especially Crohn's disease,
 XX multiple sclerosis and rheumatoid arthritis. They can also be used in the
 XX manufacture of a pharmaceutical composition to treat human IL-12
 XX disorders
 XX Sequence 98 AA;
 XX Query Match 54.8%; Score 63; DB 3; Length 98;
 XX Best Local Similarity 100.0%; Fred. No. 2.4e-53;
 XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVY 95
 Db 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVY 95
 QY 96 CAR 98
 Db 96 CAR 98
 RESULT 11
 ID AAB40101 standard; protein; 98 AA.
 XX AAB40101;
 AC

XX 05-FEB-2001 (first entry)
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 627.
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 XX complementarity determining region; CDR; antirheumatic; antiarthritic;
 XX antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX Homo sapiens.
 XX WO200056772-A1.
 XX 28-SEP-2000.
 XX 24-MAR-2000; 2000WO-US007946.
 XX 25-MAR-1999; 99US-0126603P.
 XX (BADI) BASF AG.
 XX (GEMY) GENETICS INST INC.
 XX Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M;
 XX Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A; AR;
 XX Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 XX Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.
 XX New human antibody specific for human interleukin-12 (IL-12) used to
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 XX disease and multiple sclerosis.
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 XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
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 XX region (CDR) amino acid sequences, and also includes variable region
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 XX represent other CDR sequences. Light chain CDR3 consensus sequences are
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 XX binding fragments are useful in the treatment of disorders associated
 XX with detrimental release of human IL-12, especially Crohn's disease,
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 XX disorders
 XX Sequence 98 AA;
 XX Query Match 54.8%; Score 63; DB 3; Length 98;
 XX Best Local Similarity 100.0%; Fred. No. 2.4e-53;
 XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVY 95
 Db 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVY 95
 QY 96 CAR 98
 Db 96 CAR 98

RESULT 12
AAB40110
ID AAB40110 standard; protein; 98 AA.
XX
AC AAB40110;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 636.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US007946.
XX
PR 25-MAR-1999; 99US-0126603P.
XX
PA (BADI) BASF AG.
PA (GENY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
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PT disease and multiple sclerosis.
XX
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XX
SQ Sequence 98 AA;
Query Match 54.8%; Score 63; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
36 WYRQAFKGLWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVY 95
36 WYRQAFKGLWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVY 95

QY 96 CAR 98
DB 96 CAR 98
RESULT 13
AAB40117
ID AAB40117 standard; protein; 98 AA.
XX
AC AAB40117;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 643.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US007946.
XX
PR 25-MAR-1999; 99US-0126603P.
XX
PA (BADI) BASF AG.
PA (GENY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
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PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
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PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
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XX
SQ Sequence 98 AA;
Query Match 54.8%; Score 63; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRADETAVYY 95
 |||||
 Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRADETAVYY 95
 |||||
 QY 96 CAR 98
 |||||
 Db 96 CAR 98
 |||||

RESULT 14
 AAB40128
 ID AAB40128 standard; protein; 98 AA.
 XX
 AC AAB40128;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 654.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO2000056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 XX (GEMY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 DR WPI; 2000-638250/61.
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 CC disorders

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 Query Match 54.8%; Score 63; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 0;
 QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRADETAVYY 95
 |||||
 Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRADETAVYY 95
 |||||
 QY 96 CAR 98
 |||||
 Db 96 CAR 98
 |||||

RESULT 15
 AAB40099
 ID AAB40099 standard; protein; 98 AA.
 XX
 AC AAB40099;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 625.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO2000056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 XX (GEMY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 DR WPI; 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated

CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 CC Sequence 98 AA;
 SQ
 Query Match 54.8%; Score 63; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95
 Db 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95
 QY 96 CAR 98
 Db 96 CAR 98
 RESULT 16
 AAB40103
 ID AAB40103 standard; protein; 98 AA.
 XX
 AC AAB40103;
 DT 05-FEB-2001 (first entry)
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 629.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparastic; antidiabetic; cardiant;
 KW antiparastic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 XX WO200056772-A1.
 XX 28-SEP-2000.
 XX 24-MAR-2000; 2000WO-US007946.
 XX 25-MAR-1999; 99US-0126603P.
 XX (SADI) BASF AG.
 XX (GEMY) GENETICS INST INC.
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX WPI; 2000-638250/61.
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 PT
 PS Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAB61062-

CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antirheumatic; antisclerotic; antidiabetic; antiparastic;
 CC neuroprotective; antiparastic; antidiabetic; cardiant; antiparastic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 CC Sequence 98 AA;
 SQ

Query Match 54.8%; Score 63; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95
 Db 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95
 QY 96 CAR 98
 Db 96 CAR 98

RESULT 17
 AAB67512
 ID AAB67512 standard; peptide; 98 AA.
 XX
 AC AAB67512;
 DT 29-MAY-2001 (first entry)
 DE Heavy chain variable region of anti-CTLA-4 antibody 3-30.3.
 XX
 KW Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Region 31..35
 FT /note= "CDR1"
 XX Region 50..66
 FT /note= "CDR2"
 XX WO200114424-A2.
 XX 01-MAR-2001.
 XX 24-AUG-2000; 2000WO-US023356.
 XX 24-AUG-1999; 99US-0150452P.
 XX (MEDA-) MEDAREX INC.
 XX Korman AJ, Halk EL, Lomberg N;
 XX WPI; 2001-202933/20.
 XX Novel human sequence antibody that binds to human cytotoxic T lymphocyte
 PT associated antigen-4, useful for inducing, augmenting or prolonging
 PT immune response to antigen or for suppressing immune response in patient.
 XX
 PS Example 3; Fig 8; 127pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of human
 CC antibody 3-30.3. This antibody specifically binds to human cytotoxic T
 CC lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in

CC methods for inducing, augmenting or prolonging an immune response to an
 CC antigen in a patient, where the antibodies block binding of human CTLA-4
 CC to human B7 ligands. The antibodies are also useful for treating
 CC autoimmune disease in a subject caused or exacerbated by increased
 CC activity of T cells and for treating prostate cancer, melanoma or
 CC epithelial cancer. A polyvalent or polyclonal antibody preparation
 CC comprising two antibodies of the invention are useful for suppressing a
 CC immune response in a patient. They are used for treating cancer,
 CC infectious diseases and promoting beneficial autoimmune reactions for the
 CC treatment of diseases with inflammatory or allergic components. The
 CC polyvalent or polyclonal preparations are useful for treating autoimmune
 CC diseases such as rheumatoid arthritis, myasthenia gravis and lupus
 CC erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus,
 CC transplant rejection, and inflammation, graft versus host disease
 XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 4; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVISYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYY 95
 DB |||||
 QY 36 WVRQAPGKLEWVAIVISYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYY 95
 DB |||||

RESULT 18
 AAB67507
 ID AAB67507 standard; peptide, 98 AA.
 AC AAB67507;
 DT 29-MAY-2001 (first entry)
 DE Light chain variable region of anti-CTLA-4 antibody 3-30-3.
 XX Complementarity determining region; CDR; immune response; antibody;
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
 KW autoimmune disease; infectious disease; inflammation; allergy;
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
 KW transplant rejection; graft versus host disease.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 XX
 FN WO200114424-A2.
 XX
 PD 01-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-US023356.
 XX
 PR 24-AUG-1999; 99US-0150452P.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Korman AJ, Halk EL, Lonberg N;
 XX WPI; 2001-202933/20.
 DR Novel human sequence antibody that binds to human cytotoxic T lymphocyte
 XX associated antigen-4, useful for inducing, augmenting or prolonging
 PT immune response to antigen or for suppressing immune response in patient.
 XX

Example 3; Fig 7; 127pp; English.

PS The present sequence represents the light chain variable region of human
 XX antibody 10P1. This antibody specifically binds to human cytotoxic T
 CC lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in
 CC methods for inducing, augmenting or prolonging an immune response to an
 CC antigen in a patient, where the antibodies block binding of human CTLA-4
 CC to human B7 ligands. The antibodies are also useful for treating
 CC autoimmune disease in a subject caused or exacerbated by increased
 CC activity of T cells and for treating prostate cancer, melanoma or
 CC epithelial cancer. A polyvalent or polyclonal antibody preparation
 CC comprising two antibodies of the invention are useful for suppressing a
 CC immune response in a patient. They are used for treating cancer,
 CC infectious diseases and promoting beneficial autoimmune reactions for the
 CC treatment of diseases with inflammatory or allergic components. The
 CC polyvalent or polyclonal preparations are useful for treating autoimmune
 CC diseases such as rheumatoid arthritis, myasthenia gravis and lupus
 CC erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus,
 CC transplant rejection, and inflammation, graft versus host disease
 XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 4; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVISYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYY 95
 DB |||||
 QY 36 WVRQAPGKLEWVAIVISYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYY 95
 DB |||||

RESULT 19
 ABG78201
 ID ABG78201 standard; protein, 98 AA.
 XX
 AC ABG78201;
 DT 15-NOV-2002 (first entry)
 XX Human Fv molecule hypervariable region related peptide #76.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX Homo sapiens.
 OS
 XX WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Feretz T;
 XX WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 or fragment, or construct of fragment with enhanced binding
 characteristics so as to selectively bind target cell in favor of other
 cells.

Claim 13; Page 186; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95
 DB 36 WVRQAPGKLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95

QY 96 CAR 98
 DB 96 CAR 98

RESULT 20
 ABG78199
 ID ABG78199 standard; protein; 98 AA.
 AC ABG78199;
 XX
 XX 15-NOV-2002 (first entry)
 DE Human Fv molecule hypervariable region related peptide #74.
 XX
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 XX Homo sapiens.
 OS
 XX WO200259264-A2.
 PN
 XX 01-AUG-2002.
 PD
 XX 31-DEC-2001; 2001WO-US049440.
 PF
 XX 29-DEC-2000; 2000US-00751181.
 PR
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 PI
 XX WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 or fragment, or construct of fragment with enhanced binding
 characteristics so as to selectively bind target cell in favor of other
 cells.
 PS
 XX Claim 13; Page 185; 232pp; English.

The invention relates to a peptide or polypeptide comprising an Fv
 molecule, a construct or fragments or a construct of a fragment with
 enhanced binding characteristics which selectively and/or specifically
 binds to a target cell in favour of other cells, where binding is

CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95
 DB 36 WVRQAPGKLEWVAISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95

QY 96 CAR 98
 DB 96 CAR 98

RESULT 21
 ABG78200
 ID ABG78200 standard; protein; 98 AA.
 AC ABG78200;
 XX
 XX 15-NOV-2002 (first entry)
 DE Human Fv molecule hypervariable region related peptide #75.
 XX
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 XX Homo sapiens.
 OS
 XX WO200259264-A2.
 PN
 XX 01-AUG-2002.
 PD
 XX 31-DEC-2001; 2001WO-US049440.
 PF
 XX 29-DEC-2000; 2000US-00751181.
 PR
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 PI
 XX WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 or fragment, or construct of fragment with enhanced binding
 characteristics so as to selectively bind target cell in favor of other
 cells.
 PS
 XX Claim 13; Page 186; 232pp; English.

The invention relates to a peptide or polypeptide comprising an Fv
 molecule, a construct or fragments or a construct of a fragment with
 enhanced binding characteristics which selectively and/or specifically
 binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 SQ Sequence 98 AA;
 Query Match 54.8%; Score 63; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WYRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
 Db 36 WYRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
 QY 96 CAR 98
 Db 96 CAR 98
 RESULT 22
 ABG91890
 ID ABG91890 standard; protein; 98 AA.
 AC ABG91890;
 DT 04-DEC-2002 (first entry)
 DE Human antibody fragment #74.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 PS
 PS Disclosure; Page 262; Opp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 SQ Sequence 98 AA;
 Query Match 54.8%; Score 63; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WYRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
 Db 36 WYRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
 QY 96 CAR 98
 Db 96 CAR 98
 RESULT 23
 ABG91891
 ID ABG91891 standard; protein; 98 AA.
 AC ABG91891;
 DT 04-DEC-2002 (first entry)
 DE Human antibody fragment #75.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 PS
 PS Disclosure; Page 262-263; Opp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one

antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumor or leukemia cells, increase in number of tumor or leukemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumor or leukemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukemia agents, or for decreasing the number of tumor or leukemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRADTAVYY 95
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRADTAVYY 95
QY 96 CAR 98
DB 96 CAR 98

RESULT 24

ABG91892
ID ABG91892 standard; protein; 98 AA.

AC ABG91892;

DT 04-DEC-2002 (first entry)

DE Human antibody fragment #76.

Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.

PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H, Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A, WPI; 2002-674776/72.

Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.

PS Disclosure; Page 263; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumor or leukemia cells, increase in number of tumor or leukemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumor or leukemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukemia agents, or for decreasing the number of tumor or leukemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRADTAVYY 95
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRADTAVYY 95
QY 96 CAR 98
DB 96 CAR 98

RESULT 25

ABO27091
ID ABO27091 standard; protein; 98 AA.

AC ABO27091;

DT 10-SEP-2003 (first entry)

DE Human germline heavy chain variable region gene segment #24.

Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type.

OS Homo sapiens.

PN US2003039649-A1.

PD 27-FEB-2003.

PF 12-JUL-2002; 2002US-00194975.

PR 12-JUL-2001; 2001US-0305111P.

PA (FOOT/) FOOTE J.

PI Foote J;

DR WPI; 2003-492151/46.

Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.

PS Example 1; Fig 1; 31pp; English.

XX The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human heavy chain variable region gene segment used in the
 CC creation of humanised antibodies
 XX SQ Sequence 98 AA;

Query Match 54.8%; Score 63; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	36	WVRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNSLRADTAVYY	95
Qy	96	CAR 98	
Db	96	CAR 98	

Search completed: March 15, 2004, 07:38:13
 Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:36:38 ; Search time 22 Seconds
(without alignments) 269.863 Million cell u

Title: US-09-620-9558-2

Perfect score:

Sequence: 1 QVQLQESGGGLVQPGGSLRL...CARDRYFDLWGRGTLVTSS 115

Scoring table: OLIGO
Gapop 60.0 ; Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size :

Total number of hits satisfying chosen parameters: 274646

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Minimum DB seq length: 0
Maximum DB seq length: 115
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Maximum DB seq length: 173

Post-processing: Listing first 100 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pcp.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	46	54.8	98	1	US-08-211-202-118	Sequence 12, App	
2	63	40.0	89	4	US-09-473-087-72	Sequence 78, Appl	
3	40	34.8	95	3	US-09-043-514-2	Sequence 2, Appl	
4	40	34.8	113	3	US-08-974-896-5	Sequence 6, Appl	
5	32	27.8	32	1	US-08-471-760C-82	Sequence 82, Appl	
6	32	27.8	32	1	US-08-467-282B-82	Sequence 82, Appl	
7	32	27.8	32	2	US-08-471-282A-82	Sequence 82, Appl	
8	32	27.8	32	2	US-08-466-710C-82	Sequence 82, Appl	
9	32	27.8	32	2	US-08-470-139-21	Sequence 21, Appl	
10	32	27.8	32	3	US-08-468-739C-82	Sequence 82, Appl	
11	32	27.8	32	4	US-09-347-061-21	Sequence 21, Appl	
12	31	27.0	32	1	US-07-988-935-9	Sequence 9, Appl	
13	31	27.0	32	2	US-08-362-780-9	Sequence 9, Appl	
14	31	27.0	87	1	US-08-499-312-21	Sequence 21, Appl	
15	29	25.2	98	1	US-08-211-202-116	Sequence 116, App	
16	29	25.2	112	1	US-08-211-202-133	Sequence 133, App	
17	28	24.3	111	1	US-08-211-202-134	Sequence 134, App	
18	27	23.5	98	1	US-07-943-245-37	Sequence 37, Appl	
19	27	23.5	98	2	US-08-428-197-48	Sequence 48, Appl	
20	27	23.5	98	2	US-08-665-202-31	Sequence 31, Appl	
21	27	23.5	98	4	US-09-315-574-31	Sequence 31, Appl	
22	27	23.5	98	5	PCI-08933-10355-48	Sequence 48, Appl	
23	26	22.6	110	1	US-08-211-202-117	Sequence 117, App	
24	26	22.6	111	4	US-09-266-805-6	Sequence 6, Appl	
25	25	21.7	30	1	US-07-988-945-7	Sequence 7, Appl	
26	25	21.7	30	2	US-08-362-780-7	Sequence 7, Appl	
27	25	21.7	30	2	US-08-765-783A-92	Sequence 92, Appl	

ALIGNMENTS

RESULT 1

US-08-211-202-118
; Sequence 118, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPER, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/POCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-118

Query Match 54.8%; Score 63; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.2e-48;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYY 95
DB 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYY 95

QY 96 CAR 98
DB 96 CAR 98

RESULT 2

US-09-472-087-72
; Sequence 72, Application US/09472087
; Patent No. 6582736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-72

Query Match 40.0%; Score 46; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 YDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYYCAR 98
DB 44 YDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYYCAR 89

RESULT 3

US-09-043-514-2
; Sequence 2, Application US/09043514A
; Patent No. 6153745
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, David
; APPLICANT: BROWN, Daniel
; APPLICANT: ZACCOLO, Manuela C.
; APPLICANT: GHERARDI, Ezmanac
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MUTAGENESIS OF NUCLEIC
; FILE REFERENCE: 41301/251704
; CURRENT APPLICATION NUMBER: US/09/043,514A
; CURRENT FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: GB 9519425.4
; EARLIER FILING DATE: 1995-09-22
; EARLIER APPLICATION NUMBER: GB 9602011.0
; EARLIER FILING DATE: 1996-02-01
; EARLIER APPLICATION NUMBER: PCT/GB96/02333
; EARLIER FILING DATE: 1996-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; FEATURE:
; OTHER INFORMATION: Primer
US-09-043-514-2

Query Match 34.8%; Score 40; DB 3; Length 95;

Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YVADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAR 98
Db |||||
53 YVADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAR 92
|||

RESULT 4
US-08-974-899-6
; Sequence 6, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Gardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-974-899-6

Query Match 34.8%; Score 40; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.3e-28;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YVADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAR 98
Db |||||
53 YVADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAR 98
|||

RESULT 5
US-08-471-780C-82
; Sequence 82, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.

COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,780C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-780C-82

Query Match 27.8%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 RFTISRDNSKNTLYLQMNSLRAEDTAVYCAR 98
Db |||||
1 RFTISRDNSKNTLYLQMNSLRAEDTAVYCAR 32
|||

RESULT 6
US-08-467-282B-82
; Sequence 82, Application US/08467282B
; Patent No. 580988
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0

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; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-282B-82

Query Match      27.8%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 7
US-08-471-282A-82
; Sequence 82, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-710C-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 9
US-08-466-710C-82
; Sequence 82, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-710C-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 9
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-282A-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 8
US-08-466-710C-82
; Sequence 82, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-710C-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 9
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US-08-470-139-21
; Sequence 21, Application US/08470139
; Patent No. 599585
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,139
; FILING DATE: 06 JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TRUJILLO, DOREEN YATKO
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0044
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-139-21

Query Match 27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RTISRDNSKNTLYLQMSLRADTAVYYCAR 98
Db 1 RTISRDNSKNTLYLQMSLRADTAVYYCAR 32

RESULT 10
US-08-468-739C-82
; Sequence 82, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Gasterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,739C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.

; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-739C-82

Query Match 27.8%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RTISRDNSKNTLYLQMSLRADTAVYYCAR 98
Db 1 RTISRDNSKNTLYLQMSLRADTAVYYCAR 32

RESULT 11
US-09-347-061-21
; Sequence 21, Application US/09347061
; Patent No. 6316227
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0071
; CURRENT APPLICATION NUMBER: US/09/347,061
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus
US-09-347-061-21

Query Match 27.8%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RTISRDNSKNTLYLQMSLRADTAVYYCAR 98
Db 1 RTISRDNSKNTLYLQMSLRADTAVYYCAR 32

RESULT 12
US-07-988-925-9
; Sequence 9, Application US/07988925
; Patent No. 5585097
; GENERAL INFORMATION:
; APPLICANT: Bolt, Sarah L
; APPLICANT: Clark, Michael R
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: antibody preparation
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye pc
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA

ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/07/988,925
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/01933
FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-988-925-9

Query Match 27.0%; Score 31; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RFTISRDNSKNTLYLQMNLSRAEDTAVYYCA 97
|||||
Db 1 RFTISRDNSKNTLYLQMNLSRAEDTAVYYCA 31

RESULT 13
US-08-362-780-9
Sequence 9, Application US/08362780
Patent No. 5968509
GENERAL INFORMATION:
APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: Antibody Preparation
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye pc
STREET: 8th Floor, 1100 No. 5968509th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/362,780
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/862,543
FILING DATE: 23-JUNE-1992
APPLICATION NUMBER: GB 9021679.7
FILING DATE: 05-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB91/01726

FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-362-780-9

Query Match 27.0%; Score 31; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 RFTISRDNSKNTLYLQMNLSRAEDTAVYYCA 97
|||||
Db 1 RFTISRDNSKNTLYLQMNLSRAEDTAVYYCA 31

RESULT 14

US-08-497-312-21
Sequence 21, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PMO4UT
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-497-312-21

Query Match 27.0%; Score 31; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 RTTISRDNSKNTLYLQMSLRAEDTAVYYCA 97
|||||
DB 45 RTTISRDNSKNTLYLQMSLRAEDTAVYYCA 75

RESULT 15

US-08-211-202-116
; Sequence 116, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPER, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELEPHONE: 312-474-0448
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-116

Query Match 25.2%; Score 29; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ESGGGLVPGGSLRLSCAASGFTFSYSM 34
|||||

Db 6 ESGGGLVPGGSLRLSCAASGFTFSYSM 34

RESULT 16

US-08-211-202-133
; Sequence 133, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPER, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-133

Query Match 25.2%; Score 29; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 2e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ESGGGLVPGGSLRLSCAASGFTFSYSM 34
|||||

Db 6 ESGGGLVPGGSLRLSCAASGFTFSYSM 34

RESULT 17

US-08-211-202-134
; Sequence 134, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENDOORN, Hendricus Renerus Jacobus Mattheus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPER, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-134

Query Match 24.3%; Score 28; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGLVQPGSLRLSCAASGTFSSY 34

DB 7 SGGLVQPGSLRLSCAASGTFSSY 34

RESULT 18

US-07-942-245-37
; Sequence 37, Application US/07942245
; Patent No. 5639641

GENERAL INFORMATION:

; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-07-942-245-37

Query Match 23.5%; Score 27; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGLVQPGSLRLSCAASGTFSSY 32

DB 6 ESGGLVQPGSLRLSCAASGTFSSY 32

RESULT 19

US-08-428-197-48
; Sequence 48, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:

; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:

```
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/10555
/ FILING DATE: 29-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Howells, Stacy L.
/ REGISTRATION NUMBER: 34,842
/ REFERENCE/DOCKET NUMBER: FD-2630
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 455-5100
/ TELEFAX: (619) 455-5110
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-428-197-48

Query Match 23.5%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32
Db 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 20
US-08-665-202-31
/ Sequence 31, Application US/08665202
/ Patent No. 597322
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schier, Robert
/ TITLE OF INVENTION: No. 597322el High Affinity Human Antibodies to
/ TITLE OF INVENTION: Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 13-JUN-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION NUMBER: US 60/000,238
/ APPLICATION DATE: 14-JUN-1995
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION NUMBER: US 60/000,250
/ APPLICATION DATE: 15-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061410
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: linear
/ MOLECULE TYPE: peptide
US-08-428-197-48

Query Match 23.5%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32
Db 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 21
US-09-315-574-31
/ Sequence 31, Application US/09315574
/ Patent No. 6512097
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schier, Robert
/ TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
/ TITLE OF INVENTION: Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
/ STREET: Four Embarcadero Center, Suite 1100
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-4106
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 20-MAY-99
/ CLASSIFICATION: 530
/ PRIOR APPLICATION NUMBER: US/09/315.574
/ APPLICATION DATE: 14-JUN-1995
/ FILING DATE: 15-JUN-1995
/ PRIOR APPLICATION NUMBER: US 60/000,250
/ APPLICATION DATE: 13-JUN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061411
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: linear
/ MOLECULE TYPE: peptide
US-09-315-574-31

Query Match 23.5%; Score 27; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32
Db 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 22
PCT-US93-10555-48
```

```
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/10555
/ FILING DATE: 29-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Howells, Stacy L.
/ REGISTRATION NUMBER: 34,842
/ REFERENCE/DOCKET NUMBER: FD-2630
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 455-5100
/ TELEFAX: (619) 455-5110
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-428-197-48

Query Match 23.5%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32
Db 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 20
US-08-665-202-31
/ Sequence 31, Application US/08665202
/ Patent No. 597322
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schier, Robert
/ TITLE OF INVENTION: No. 597322el High Affinity Human Antibodies to
/ TITLE OF INVENTION: Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 13-JUN-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION NUMBER: US 60/000,238
/ APPLICATION DATE: 14-JUN-1995
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION NUMBER: US 60/000,250
/ APPLICATION DATE: 15-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061410
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: linear
/ MOLECULE TYPE: peptide
US-08-428-197-48

Query Match 23.5%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32
Db 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 21
US-09-315-574-31
/ Sequence 31, Application US/09315574
/ Patent No. 6512097
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schier, Robert
/ TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
/ TITLE OF INVENTION: Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
/ STREET: Four Embarcadero Center, Suite 1100
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-4106
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 20-MAY-99
/ CLASSIFICATION: 530
/ PRIOR APPLICATION NUMBER: US/09/315.574
/ APPLICATION DATE: 14-JUN-1995
/ FILING DATE: 15-JUN-1995
/ PRIOR APPLICATION NUMBER: US 60/000,250
/ APPLICATION DATE: 13-JUN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061411
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: linear
/ MOLECULE TYPE: peptide
US-09-315-574-31

Query Match 23.5%; Score 27; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32
Db 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 22
PCT-US93-10555-48
```


Sequence 48, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Juba & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10555-48

Query Match 23.5%; Score 27; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGSLRLSCAASGFTFSY 32
Db 6 ESGGGLVQPGSLRLSCAASGFTFSY 32

RESULT 23
US-08-211-202-117
Sequence 117, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOGENBOOM, Hendricus Renerus Jacobus Mattheus
APPLICANT: BAER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-117

Query Match 22.6%; Score 26; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGSLRLSCAASGFTFSY 32
Db 7 SGGGLVQPGSLRLSCAASGFTFSY 32

RESULT 24
US-09-266-805-6
Sequence 6, Application US/09266805
Patent No. 6517829
GENERAL INFORMATION:
APPLICANT: Unilever N.V.
APPLICANT: Unilever PLC
TITLE OF INVENTION: New products comprising inactivated yeasts or moulds
TITLE OF INVENTION: provided with active antibodies
FILE REFERENCE: t-7055
CURRENT APPLICATION NUMBER: US/09/266,805
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 111
TYPE: PRT
ORGANISM: llama
US-09-266-805-6

Query Match 22.6%; Score 26; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGGGLVQPGSLRLSCAASG 26
Db 1 QVQLQESGGGLVQPGSLRLSCAASG 26

RESULT 25
US-07-988-925-7
; Sequence 7, Application US/07988925
; Patent No. 5585097
; GENERAL INFORMATION:
; APPLICANT: Bolt, Sarah L
; APPLICANT: Clark, Michael R
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: antibody preparation
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye PC
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,925
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206422.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB92/01933
; FILING DATE: 21-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-988-925-7

Query Match 21.7%; Score 25; DB 1; Length 30;
Best Local Similarity 100.0%; Pred.No. 2.3e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 BSGGGLVOPGGSLRLSCAASGFTFS 30
|||
DB 6 BSGGGLVOPGGSLRLSCAASGFTFS 30
|||

Search completed: March 15, 2004, 07:40:10
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:29:38 ; Search time 20 Seconds
(without alignments)
553.101 Million cell updates/sec

Title: US-09-620-955B-2

Perfect score: 115

Sequence: 1 QVQLQESGGGLVQPGGSLRL.....CARDRYFDLWGRGLTVTVSS 115

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191536 residues

Word size : 0

Total number of hits satisfying chosen parameters: 48432

Minimum DB seq length: 0

Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database :

PTR-78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	56.5	111	2 PH1645	Ig heavy chain V r
2	64	55.7	109	2 PH1646	Ig heavy chain V r
3	64	55.7	114	2 S46390	Ig heavy chain V r
4	64	55.7	114	2 S46392	Ig heavy chain V r
5	63	54.8	98	2 S29546	Ig heavy chain V r
6	63	54.8	109	2 PH1644	Ig heavy chain V r
7	62	53.9	98	2 PLO116	Ig heavy chain V-I
8	62	53.9	111	2 PH1643	Ig heavy chain V r
9	60	52.2	97	2 S44115	Ig heavy chain V r
10	59	51.3	94	2 PLO120	Ig heavy chain V-I
11	47	40.9	108	2 PH1642	Ig heavy chain V r
12	47	40.9	114	2 S46391	Ig heavy chain V r
13	45	39.1	98	2 S29543	Ig heavy chain V r
14	40	34.8	97	2 S26935	Ig heavy chain V r
15	40	34.8	97	2 S46462	Ig heavy chain V r
16	40	34.8	105	2 S24249	Ig heavy chain V r
17	39	33.9	98	2 S26893	Ig heavy chain V r
18	39	33.9	99	2 S42253	Ig heavy chain V r
19	39	33.9	100	2 S42258	Ig heavy chain V r
20	39	33.9	101	2 S42257	Ig heavy chain V r
21	39	33.9	102	2 S24255	Ig heavy chain V r
22	39	33.9	104	2 S24255	Ig heavy chain V r
23	39	33.9	106	2 S24256	Ig heavy chain V r
24	39	33.9	108	2 PH1648	Ig heavy chain V r
25	39	33.9	109	2 PH1649	Ig heavy chain V r
26	39	33.9	110	2 S69897	Ig heavy chain V r
27	39	33.9	112	2 PH1647	Ig heavy chain V r
28	39	33.9	113	2 S38490	Ig heavy chain - h
29	38	33.0	96	2 S20781	Ig heavy chain V r

30	31.3	52	2	S21591	Ig heavy chain V r
31	31.3	113	2	S24247	Ig heavy chain V r
32	34	76	2	S31592	Ig heavy chain V r
33	28.7	90	2	S24248	Ig heavy chain V r
34	31	115	2	S36284	Ig heavy chain V r
35	29	98	2	S26894	Ig heavy chain V r
36	29	105	2	S38488	Ig heavy chain - h
37	27	97	2	PH0872	Ig heavy chain V r
38	27	97	2	S26890	Ig heavy chain V r
39	27	98	2	PL0121	Ig heavy chain V-I
40	27	98	2	PL0123	Ig heavy chain V-I
41	27	98	2	S26896	Ig heavy chain V r
42	27	98	2	S29545	Ig heavy chain V r
43	27	98	2	S26891	Ig heavy chain V r
44	27	113	2	S25571	Ig heavy chain V r
45	27	114	2	S36280	Ig heavy chain V r
46	26	101	2	JT0511	Ig heavy chain V-I
47	25	98	2	S26933	Ig heavy chain V r
48	25	98	2	S26934	Ig heavy chain V r
49	25	100	2	S28925	Ig heavy chain V r
50	25	100	2	S28926	Ig heavy chain V r
51	25	109	2	S24254	Ig heavy chain V r
52	25	115	1	H3HUTL	Ig heavy chains V-
53	24	111	2	PH1659	Ig heavy chain V r
54	23	114	2	PH1657	Ig heavy chain V r
55	22	114	2	PH1658	Ig heavy chain pre
56	21	82	2	C34964	Ig heavy chain V r
57	21	98	2	S26940	Ig heavy chain V r
58	21	108	2	PH1651	Ig heavy chain V r
59	21	109	2	PH1653	Ig heavy chain V r
60	21	110	2	PH1652	Ig heavy chain V r
61	20	63	2	S26796	Ig heavy chain V r
62	20	97	2	PH0875	Ig heavy chain V r
63	20	98	2	S28930	Ig heavy chain V r
64	20	108	2	S24251	Ig heavy chain V r
65	20	110	2	PH1655	Ig heavy chain V r
66	20	110	2	S36282	Ig heavy chain V r
67	20	115	2	S20706	Ig heavy chain V r
68	19	98	2	S26929	Ig heavy chain V r
69	19	98	2	S54854	Ig heavy chain V r
70	19	108	2	PH1656	Ig heavy chain V r
71	19	110	2	S24250	Ig heavy chain V r
72	19	114	1	AVD3GM	Ig heavy chain V r
73	19	114	2	S31120	Ig heavy chain - h
74	18	70	2	S20770	Ig heavy chain V r
75	18	96	2	S54854	Ig heavy chain V r
76	17	97	2	S28885	Ig heavy chain V r
77	17	97	2	S28886	Ig heavy chain V r
78	17	98	2	S26932	Ig heavy chain V r
79	17	99	2	S20765	Ig heavy chain V r
80	17	113	2	S25575	Ig heavy chain V r
81	17	113	2	S25573	Ig heavy chain V r
82	17	115	1	G3HUNJ	Ig heavy chain V-I
83	17	115	2	S57445	Ig heavy chain V-I
84	16	58	2	S31683	Ig heavy chain V r
85	16	95	2	S20777	Ig heavy chain V r
86	16	97	2	S24252	Ig heavy chain V r
87	16	98	2	PH0874	Ig heavy chain V r
88	16	98	2	S26928	Ig heavy chain V r
89	16	98	2	F47624	Ig heavy chain V-I
90	16	115	1	A2HUBU	Ig heavy chain V-I
91	16	115	2	S09382	Ig heavy chain - c
92	15	34	2	S46474	Ig heavy chain V r
93	15	38	2	S33402	Ig heavy chain V r
94	15	60	2	S36382	Ig heavy chain V r
95	15	96	2	PH0873	Ig heavy chain V r
96	15	100	2	S26927	Ig heavy chain V r
97	15	100	2	S63896	Ig heavy chain V r
98	15	106	2	S37454	Ig mu chain - huma
99	15	110	2	PH1674	Ig heavy chain V r
100	15	112	2	PH1654	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1645
R:Hallson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1645
A:Accession: PH1645
A:Molecule type: mRNA
A:Residues: 1-111 <HL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 55.5%; Score 65; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95
DB 28 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 87

QY 96 CARD 100
DB 88 CARD 92

RESULT 2

PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1646
R:Hallson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1646; MUID:93301610; PMID:8315388
A:Accession: PH1646
A:Molecule type: mRNA
A:Residues: 1-109 <HL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 64; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.8e-58;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95
DB 28 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 87

QY 96 CARD 99
DB 88 CARD 91

RESULT 3

S46390
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46390
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048

A:Accession: S46390
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31686; NID:G509782; PIDN:CAA83493.1; PID:gl335143
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 5e-58;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95
DB 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95

QY 96 CARD 99
DB 96 CARD 99

RESULT 4

S46392
Ig heavy chain V region (VH-28) - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46392
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46392
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31688; NID:G499306; PIDN:CAA83493.1; PID:gl335145
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 5e-58;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95
DB 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95

QY 96 CARD 99
DB 96 CARD 99

RESULT 5

S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29546; S26888
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29546
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PID:G32844
A>Note: Designated COS-8
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline VH sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26888

Query Match 55.7%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 5e-58;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95
DB 36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95

QY 96 CARD 99
DB 96 CARD 99

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOW>
A;Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMW>

Query Match 54.8%; Score 63; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.7e-57;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 95
|||
DB 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 95
|||

QY 96 CAR 98
|||
DB 96 CAR 98
|||

RESULT 6
PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1644
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1644; MUID:93301610; PMID:8315388
A;Accession: PH1644
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMW>

Query Match 54.8%; Score 63; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.1e-57;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 95
|||
DB 28 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 87
|||

QY 96 CAR 98
|||
DB 88 CAR 90
|||

RESULT 7
PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0116; S26892
R;Bird, J.; Gallil, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin V region
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0116
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-788, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V region segments
A;Reference number: S26895; MUID:93021117; PMID:1404388
A;Accession: S26892
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-98 <TOW>
A;Cross-references: EMBL:Z12349; NID:G32918; PIDN:CAA78219.1; PID:G32919
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMW>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Query Match 53.9%; Score 62; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 5e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 95
|||
DB 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 95
|||

QY 96 CA 97
|||
DB 96 CA 97
|||

RESULT 8
PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1643
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1643
A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMW>

Query Match 53.9%; Score 62; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 5.5e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 95
|||
DB 28 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYY 87
|||

QY 96 CA 97
|||
DB 88 CA 89
|||

RESULT 9
S44115
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44115
R;Hawkins, R.E.; Zhu, D.; Oveska, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable region
A;Reference number: S44105
A;Accession: S44115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <HAW>
A;Cross-references: EMBL:Z31384; NID:G472969; PIDN:CAA93259.1; PID:G940526
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 52.2%; Score 60; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.5e-54;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYY 95
 Db 36 WVRQAPGKLEWAVVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYY 95

RESULT 10

PL0120
 IG heavy chain V-III region (TD-Vo) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
 C:Accession: PL0120
 R:Bird, J.; Gallili, N.; Link, M.; Stites, D.; Sklar, J.
 J. Exp. Med. 168, 229-245, 1988
 A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
 A:Reference number: PL0116; MUID:88285083; PMID:2840480
 A:Accession: PL0120
 A:Molecule type: mRNA
 A:Residues: 1-94 <BIR>
 A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
 A>Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
 F:31-35/Region: complementarity-determining 1
 F:49-65/Region: complementarity-determining 2

Query Match 51.3%; Score 59; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 5.7e-53;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 94
 Db 36 WVRQAPGKLEWAVVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 94

RESULT 11

PH1642
 IG heavy chain V region (clone 5A10) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1642
 R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
 A:Reference number: PH1642; MUID:93301610; PMID:8315388
 A:Accession: PH1642
 A:Molecule type: mRNA
 A:Residues: 1-108 <HIL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 40.9%; Score 47; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e-40;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 99
 Db 45 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 91

RESULT 12

S46391
 IG heavy chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S46391
 R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
 J. Mol. Biol. 239, 68-78, 1994
 A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
 A:Reference number: S46390; MUID:94254092; PMID:8196048
 A:Accession: S46391
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-114 <FIG>
 A:Cross-references: EMBL:Z31687; NID:G509784; PIDN:CAA83492.1; PID:gl335144
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-96/Domain: immunoglobulin homology <IMM>

Query Match 40.9%; Score 47; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.3e-40;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 99
 Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 99

RESULT 13

S29543
 IG heavy chain V region (COS 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S29543
 R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S29543
 A:Accession: S29543
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 A:Cross-references: EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:G32836
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 45; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCA 97
 Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCA 97

RESULT 14

S26935
 IG heavy chain V region (DP-42) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26935
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
 A:Reference number: S26885; MUID:93021117; PMID:1404388
 A:Accession: S26935
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-97 <TOM>
 A:Cross-references: EMBL:Z12342; NID:G32905; PIDN:CAA78212.1; PID:G32906
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 40; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCAR 98
 Db 58 YYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCAR 97

RESULT 15

S46462
 IG heavy chain V region (YAC-5) - human

C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S46462
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Win
Nature Genet. 7, 162-168, 1994
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A;Reference number: S46460; MUID:95004581; PMID:7920635
A;Accession: S46462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <COO>
A;Cross-references: EMBL:Z27504; NID:G505430; PIDN:CAA81824.1; PID:G505431
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-97/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 40; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98
Db 58 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 97

RESULT 16
S24249
IG heavy chain V region (VH26-DNI-DXP1-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1999
C;Accession: S24249
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cell
A;Reference number: S24247
A;Accession: S24249
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <STE>
A;Cross-references: EMBL:X67070
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;10-92/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 40; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98
Db 53 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 92

RESULT 17
S26889
IG heavy chain V region (DP-47) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26889
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:11404388
A;Accession: S26889
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12347; NID:G32914; PIDN:CAA78217.1; PID:G32915
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.8e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97
Db 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97

RESULT 18
S24259
IG heavy chain V region (VH26-DX1-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24259
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cell
A;Reference number: S24247
A;Accession: S24259
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <STE>
A;Cross-references: EMBL:X67067; NID:G38391; PIDN:CAA47452.1; PID:G38392
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;1-83/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97
Db 44 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 82

RESULT 19
S24258
IG heavy chain V region (VH26-DXP1-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24258
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cell
A;Reference number: S24247
A;Accession: S24258
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <STE>
A;Cross-references: EMBL:X67066; NID:G38389; PIDN:CAA47451.1; PID:G38390
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;4-86/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97
Db 47 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 85

RESULT 20
S24257
IG heavy chain V region (VH26-DXP1-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24257
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24257

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <STE>

A:Cross-references: EMBL:X67065; NID:G38387; PIDN:CAA47450.1; PID:G38388

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-93/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 54 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 92

RESULT 21

S24260

IG heavy chain V region (VH26-DAL-JH4) - human

C:Species: Homo sapiens (man)

C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S24260

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24260

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <STE>

A:Cross-references: EMBL:X67068

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:5-87/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 48 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 86

RESULT 22

S24255

IG heavy chain V region (VH26-DLR5-JH4) - human

C:Species: Homo sapiens (man)

C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S24255

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24255

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <STE>

A:Cross-references: EMBL:X67063

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:2-84/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 45 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 83

RESULT 23

S24256

IG heavy chain V region (VH26-DXP4-JH6) - human

C:Species: Homo sapiens (man)

C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S24256

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24256

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <STE>

A:Cross-references: EMBL:X67064; NID:G38385; PIDN:CAA47449.1; PID:G38386

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:4-86/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 47 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 85

RESULT 24

PH1648

IG heavy chain V region (clone 2B8) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1648

R: Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1648

A:Molecule type: mRNA

A:Residues: 1-108 <HIL>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 51 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 89

RESULT 25

PH1649

IG heavy chain V region (clone 2E7) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1649

R: Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1649

A:Molecule type: mRNA

A:Residues: 1-109 <HIL>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2e-32;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCA 97
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 Db 51 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCA 89
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Search completed: March 15, 2004, 07:39:34
 Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:37:14 ; Search time 33 Seconds
(without alignments)
735.837 Million cell updates/sec

Title: US-09-620-955B-2

Perfect score: 115

Sequence: 1 QVQLSESGGLVPGGSLRL.....CARDYFLMGRGTLTVSS 115

Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 809742 seqs, 21153259 residues

Word size : 0

Total number of hits satisfying chosen parameters: 340717

Minimum DB seq length: 0

Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database :

Published Applications:AA:
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4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
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9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
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18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	56.5	115	14	US-10-305-347A-7
2	63	54.8	98	14	US-10-194-975-24
3	63	54.8	98	15	US-10-308-817-64
4	63	54.8	98	15	US-10-032-037B-74
5	63	54.8	98	15	US-10-032-037B-74
6	63	54.8	98	15	US-10-032-037B-74
7	63	54.8	98	15	US-10-032-037B-74
8	63	54.8	98	15	US-10-032-037B-74
9	63	54.8	98	15	US-10-032-037B-74
10	63	54.8	98	15	US-10-032-037B-74
11	63	54.8	98	15	US-10-032-037B-74
12	63	54.8	98	15	US-10-032-037B-74
13	62	53.9	98	14	US-10-194-975-23
14	62	53.9	98	14	US-10-194-975-25
15	62	53.9	98	15	US-10-308-817-63
16	62	53.9	98	15	US-10-308-817-63
17	62	53.9	98	15	US-10-308-817-63
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Sequence 63, Appl
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Sequence 44343, A
Sequence 332, App
Sequence 29, Appl
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Sequence 5, Appl
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Sequence 123, App
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Sequence 278, App
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Sequence 22, Appl
Sequence 19, Appl
Sequence 10, Appl
Sequence 62, Appl
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Sequence 145, App
Sequence 53, Appl
Sequence 18, Appl
Sequence 58, Appl
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Sequence 4, Appl
Sequence 15, Appl

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90 27 23.5 98 15 US-10-308-817-55
91 27 23.5 98 15 US-10-308-817-71
92 27 23.5 98 15 US-10-308-817-75
93 27 23.5 98 15 US-10-032-037B-79
94 27 23.5 98 15 US-10-032-037B-84
95 27 23.5 98 15 US-10-032-037B-85
96 27 23.5 98 15 US-10-029-988B-79
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98 27 23.5 98 15 US-10-029-988B-85
99 27 23.5 98 15 US-10-032-423A-79
100 27 23.5 98 15 US-10-032-423A-84

ALIGNMENTS

RESULT 1
US-10-305-347A-7
; Sequence 7, Application US/10305347A
; Publication No. US20030143603A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Bernie Scallon
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5005
; CURRENT APPLICATION NUMBER: US/10/305,347A
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 7
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-347A-7

Query Match 56.5%; Score 65; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.9e-52;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
QY 96 CARDR 100
DB 96 CARDR 100

RESULT 2
US-10-194-975-24
; Sequence 24, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24

Query Match 54.8%; Score 63; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
QY 96 CAR 98
DB 96 CAR 98

RESULT 3
US-10-308-817-64
; Sequence 64, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: WJ, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-64

Query Match 54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
QY 96 CAR 98
DB 96 CAR 98

RESULT 4
US-10-032-037B-74
; Sequence 74, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 74
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-74

Query Match 54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 95
QY 96 CAR 98
DB 96 CAR 98

RESULT 5
US-10-032-037B-75
; Sequence 75, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-75

Query Match 54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db |||||
36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db |||||
96 CAR 98

RESULT 6
US-10-032-037B-76
; Sequence 76, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-76

Query Match 54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db |||||
36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db |||||
96 CAR 98

RESULT 7
US-10-029-988B-74
; Sequence 74, Application US/10029988B

Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-74

Query Match 54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db |||||
36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db |||||
96 CAR 98

RESULT 8
US-10-029-988B-75
; Sequence 75, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-75

Query Match 54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db |||||
36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db |||||
96 CAR 98

RESULT 9
US-10-029-988B-76
; Sequence 76, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

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; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-76

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 10
US-10-032-423A-74
; Sequence 74, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-74

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 11
US-10-032-423A-75
; Sequence 75, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-75

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 12
US-10-032-423A-76
; Sequence 76, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-76

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 13
US-10-194-975-23
; Sequence 23, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-194-975-23

Query Match 53.9%; Score 62; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Qy 96 CA 97
Db 96 CA 97

RESULT 14

US-10-194-975-25
; Sequence 25, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Roore Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-25

Query Match 53.9%; Score 62; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Qy 96 CA 97
Db 96 CA 97

RESULT 15

US-10-308-817-63
; Sequence 63, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-63

Query Match 53.9%; Score 62; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95

Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95

Qy 96 CA 97
Db 96 CA 97

RESULT 16

US-10-308-817-65
; Sequence 65, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-65

Query Match 53.9%; Score 62; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Qy 96 CA 97
Db 96 CA 97

RESULT 17

US-10-032-037B-80
; Sequence 80, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: V17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-80

Query Match 53.9%; Score 62; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95
Qy 96 CA 97
Db 96 CA 97

RESULT 18

US-10-029-988B-80
; Sequence 80, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-80

Query Match 53.9%; Score 62; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYY 95
DB 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYY 95
QY 96 CA 97
DB 96 CA 97

RESULT 19

US-10-032-423A-80
; Sequence 80, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-80

Query Match 53.9%; Score 62; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYY 95
DB 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYY 95
QY 96 CA 97
DB 96 CA 97

RESULT 20

US-09-791-153A-63
; Sequence 63, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:

; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-63

Query Match 53.9%; Score 62; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.2e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYY 95
DB 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYY 95
QY 96 CA 97
DB 96 CA 97

RESULT 21

US-10-078-958-7
; Sequence 7, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (22)
; OTHER INFORMATION: Variable amino acid
US-10-078-958-7

Query Match 53.0%; Score 61; DB 14; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 RQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYYCA 97
DB 23 RQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNKNTLYLQNSLRADDTAVYYCA 82
QY 98 R 98
DB 83 R 83

```
RESULT 22
US-10-194-975-26
; Sequence 26, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Pooce, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-26

Query Match      40.0%; Score 46; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98
Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98

RESULT 23
US-10-041-860-4
; Sequence 4, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-4

Query Match      40.0%; Score 46; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98
Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98

RESULT 24
US-10-041-860-283
; Sequence 283, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
```

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; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-283

Query Match      40.0%; Score 46; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98
Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98

RESULT 25
US-10-041-860-284
; Sequence 284, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-284

Query Match      40.0%; Score 46; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98
Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98

Search completed: March 15, 2004, 07:40:55
Job time : 33 secs
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:29:28 ; Search time 39 Seconds
(without alignments)
930.374 Million cell updates/sec

Title: US-09-620-955b-2

Perfect score: 115

Sequence: 1 QVLOESGGLVQPGSLRL.....CARDRYFLWGRGLIVTSS 115

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 217408

Minimum DB seq length: 0

Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 25:

- 1: sp_arChaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_Organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	39.1	113	4	Q9UL90
2	40	34.8	112	4	Q9UGP3
3	27	23.5	95	4	Q9ULB6
4	20	17.4	112	4	Q9HCC1
5	15	13.0	104	4	Q9UL87
6	11	9.6	64	11	Q9UL750
7	10	8.7	15	11	Q9QV16
8	8	7.0	109	11	Q9JLB5
9	8	7.0	109	11	Q9JL75
10	7	6.1	102	11	Q9JL79
11	7	6.1	110	11	Q9JL63
12	7	6.1	110	11	Q9JL77
13	7	6.1	111	11	Q9D9B8
14	7	6.1	114	11	Q9JLB1
15	6	5.2	16	4	Q9UC53
16	6	5.2	29	12	Q9LHB1

17	5.2	38	4	015224	O15224 homo sapien
18	5.2	44	6	Q8WNG3	Q8WNG3 pan troglod
19	5.2	58	16	Q8EV56	Q8EV56 mycoplasma
20	5.2	66	12	Q8QO63	Q8QO63 camelpox vi
21	5.2	66	12	Q9JFD1	Q9JFD1 vaccinia vi
22	5.2	67	8	Q7YN75	Q7YN75 eimeria ten
23	5.2	70	17	Q8TQ32	Q8TQ32 methanosarc
24	5.2	72	2	Q8GB47	Q8GB47 clostridium
25	5.2	73	10	Q7UZ17	Q7UZ17 rhodospirell
26	5.2	74	16	Q8H8Q8	Q8H8Q8 oryza sativ
27	5.2	78	16	Q8WB6	Q8WB6 streptococc
28	5.2	83	17	Q8THX0	Q8THX0 methanosarc
29	5.2	85	8	Q8MDL1	Q8MDL1 packera can
30	5.2	91	10	Q8HOY6	Q8HOY6 arabidopsis
31	5.2	92	10	Q8L7G7	Q8L7G7 arabidopsis
32	5.2	96	8	Q8MDN9	Q8MDN9 erechitites
33	5.2	104	16	Q31480	Q31480 bacillus su
34	5.2	105	5	Q819M3	Q819M3 chlamys far
35	5.2	105	8	Q8MDL5	Q8MDL5 senecio ang
36	5.2	106	8	Q9MFF2	Q9MFF2 beta vulgar
37	5.2	106	8	Q8MDK9	Q8MDK9 othonna cap
38	5.2	106	8	Q8MDM2	Q8MDM2 senecio ina
39	5.2	106	8	Q8HU25	Q8HU25 zosteram mar
40	5.2	106	8	Q8HU24	Q8HU24 zosteram jap
41	5.2	106	8	Q8HU23	Q8HU23 zosteram nol
42	5.2	106	8	Q8HU22	Q8HU22 zosteram nov
43	5.2	106	8	Q8HU21	Q8HU21 zosteram cap
44	5.2	106	8	Q8HU20	Q8HU20 zosteram tue
45	5.2	106	8	Q8HBN3	Q8HBN3 bradyrhizob
46	5.2	106	16	Q89BN3	Q89BN3 bombyx mori
47	5.2	107	5	Q9BLD5	Q9BLD5 senecio cin
48	5.2	107	8	Q8MDL8	Q8MDL8 senecio cin
49	5.2	107	12	Q12379	Q12379 marek's dis
50	5.2	108	8	Q8MDM0	Q8MDM0 senecio ere
51	5.2	108	8	Q8MDK5	Q8MDK5 dendrosenec
52	5.2	108	8	Q8MDQ4	Q8MDQ4 senecio amb
53	5.2	108	15	Q998Z1	Q998Z1 human immun
54	5.2	108	16	Q7VJB1	Q7VJB1 helicobacte
55	5.2	109	5	Q8T4C7	Q8T4C7 drosophila
56	5.2	109	8	Q8MDK3	Q8MDK3 blennosperm
57	5.2	109	8	Q8MDM7	Q8MDM7 senecio pal
58	5.2	109	8	Q8MDP8	Q8MDP8 senecio chr
59	5.2	109	8	Q8MDL0	Q8MDL0 packera aur
60	5.2	109	8	Q8MDP9	Q8MDP9 senecio dor
61	5.2	110	8	Q8MDK6	Q8MDK6 emilia cocc
62	5.2	111	8	Q8MDN3	Q8MDN3 senecio squ
63	5.2	111	8	Q8MDP5	Q8MDP5 pseudogynox
64	5.2	111	8	Q8MDQ5	Q8MDQ5 synotis nag
65	5.2	111	8	Q8MDQ3	Q8MDQ3 senecio pan
66	5.2	111	8	Q8MDK8	Q8MDK8 kleinia ner
67	5.2	111	8	Q8MDM4	Q8MDM4 senecio lau
68	5.2	111	8	Q8MDK7	Q8MDK7 euryops pec
69	5.2	111	8	Q8MDN0	Q8MDN0 senecio ser
70	5.2	111	8	Q8MDN7	Q8MDN7 arrhenescht
71	5.2	111	8	Q8MDP2	Q8MDP2 lorthowea i
72	5.2	111	8	Q8MDM9	Q8MDM9 senecio aca
73	5.2	111	8	Q8MDP0	Q8MDP0 gynoxys sou
74	5.2	111	8	Q8MDP4	Q8MDP4 phaneroglos
75	5.2	111	16	Q88F31	Q88F31 pseudomonas
76	5.2	112	8	Q8MDL4	Q8MDL4 senecio ane
77	5.2	112	8	Q8MDL7	Q8MDL7 senecio art
78	5.2	112	8	Q8MDL3	Q8MDL3 senecio ado
79	5.2	112	8	Q8MDM6	Q8MDM6 senecio nem
80	5.2	112	8	Q8MDQ0	Q8MDQ0 senecio car
81	5.2	112	8	Q8MDN4	Q8MDN4 senecio vis
82	5.2	112	8	Q8MDM8	Q8MDM8 senecio row
83	5.2	112	8	Q8MDN1	Q8MDN1 senecio sub
84	5.2	113	8	Q8VDO1	Q8VDO1 senecio min
85	5.2	114	2	Q8VY89	Q8VY89 terrabacter
86	5.2	114	8	Q8MDM5	Q8MDM5 senecio med
87	5.2	114	8	Q8VND2	Q8VND2 senecio syl
88	5.2	114	8	Q8VDM1	Q8VDM1 senecio eru
89	5.2	114	8	Q8MDL6	Q8MDL6 senecio aqu

90 6 5.2 114 12 Q911W9
91 6 5.2 114 12 Q911W7
92 6 5.2 114 12 Q911W8
93 6 5.2 114 12 Q911W6
94 6 5.2 114 12 Q911W5
95 6 5.2 114 15 P88783
96 6 5.2 114 16 Q9JWD0
97 6 5.2 115 8 Q9GLH0
98 6 5.2 115 8 Q9G9Y9
99 6 5.2 115 8 Q63905
100 6 5.2 115 8 Q953K0

Q911W9 human polio
Q911W7 human polio
Q911W8 human polio
Q911W6 human polio
Q911W5 human polio
P88783 human immun
Q9JWD0 neisseria m
Q9GLH0 eulemur ful
Q9G9Y9 eulemur ful
Q63905 myoxus glis
Q953K0 ochotona co

ALIGNMENTS

RESULT 1
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035024; AAD56260.1; --
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
Query Match 39.1%; Score 45; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.5e-39;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 YDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 97
Db 53 YDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 97
RESULT 2
Q9UGP3 PRELIMINARY; PRT; 112 AA.
AC Q9UGP3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain (Fragment)
DE IGH.
GN IGH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zafiroopoulos A., Kandilogianaki M., Dahlenborg C., Borrebaeck C.A.K.,
Krambovitis E.;
RT "Induction of somatic mutations in human B cells by in vitro
immunization";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132560; CAB65078.1; --
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;
Query Match 34.8%; Score 40; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.7e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 YADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 99
Db 43 YADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 82
RESULT 3
Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain (Fragment)
DE VH.
GN VH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; --
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;
Query Match 23.5%; Score 27; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32
Db 5 ESGGGLVQPGGSLRLSCAASGFTFSY 31
RESULT 4
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: Isolation from a
RL human synthetic phage display library and characterization.";
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FIA45EC3B84788 CRC64;

Query Match 17.4%; Score 20; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 LXLQNSLRAEDTAVYYCAR 98
DB 79 LXLQNSLRAEDTAVYYCAR 98

RESULT 5
Q9UL87
ID Q9UL87 PRELIMINARY; PRT; 104 AA.
AC Q9UL87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035027; AAD56263.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match 13.0%; Score 15; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 YADSVKGRFTISRDN 74
DB 39 YADSVKGRFTISRDN 53

RESULT 6
Q61750
ID Q61750 PRELIMINARY; PRT; 64 AA.
AC Q61750;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE JH-Cdelta locus (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=92017847; PubMed=1922069;
RA Owens J.D.Jr., Finkelman F.D., Mountz J.D., Mushinski J.F.;
RT "Nonhomologous recombination at sites within the mouse JH-cdelta locus
RL accompanies Cmu deletion and switch to immunoglobulin D secretion.";
RL Mol. Cell. Biol. 11:5660-5670(1991).
DR EMBL; M64568; AAA39341.1; -.
DR PIR; I77394; I77394.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 64 AA; 7594 MW; FE93625079AC2F28 CRC64;

Query Match 9.6%; Score 11; DB 11; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 SVKGRFTISRD 73
DB 23 SVKGRFTISRD 33

RESULT 7
Q9QV16
ID Q9QV16 PRELIMINARY; PRT; 15 AA.
AC Q9QV16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Prolactin-binding protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RX [1]
RP SEQUENCE.
RX MEDLINE=95094032; PubMed=8000909;
RA Cohen H., Cohen O., Gagnon J.;
RT "Serum prolactin-binding protein (PRL-BP) of human and rat are
RT identified as IGF.";
RL C. R. Acad. Sci., III, Sci. Vie 317:293-298(1994).
SQ SEQUENCE 15 AA; 1469 MW; 35ED2512FF3FA369 CRC64;

Query Match 8.7%; Score 10; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 BSGGGLVQPG 15
DB 6 BSGGGLVQPG 15

RESULT 8
Q9JL85
ID Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 11944 MW; DF5615FE6CEDA4E CRC64;

Query Match 7.0%; Score 8; DB 11; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 EDTAVYVC 96
DB 81 EDTAVYVC 88

RESULT 9
Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-mysin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 12118 MW; FF5E5441B5F936A6 CRC64;

Query Match 7.0%; Score 8; DB 11; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 AVYVCARD 99
DB 83 AVYVCARD 90
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RESULT 10
Q9JL79 PRELIMINARY; PRT; 102 AA.
AC Q9JL79;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-mysin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR DR EMBL; AF206027; AAF69325.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 6.1%; Score 7; DB 11; Length 102;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 QAPGKGL 45
DB 24 QAPGKGL 30

RESULT 11
Q9JL83 PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-mysin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR DR EMBL; AF206023; AAF69321.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 1
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FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12052 MW; 84EGF2AD219AF95E CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 110;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 GILTVTS 114
Db 103 GILTVTS 109

RESULT 12
Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206029; AAF69327.1; -.
DR FIR; F33932; F33932.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 110 110
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12138 MW; 2ED81FB5862C9AF CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 110;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 AVYYCAR 98
Db 84 AVYYCAR 90

RESULT 13
Q9D9B8 PRELIMINARY; PRT; 111 AA.
AC Q9D9B8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:1700110b1, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RL EMBL; AK007163; BAB24877.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 111;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 PGKLEW 47
Db 47 PGKLEW 53

RESULT 14
Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206025; AAF69323.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 114 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA5678 CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 114;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Mon Mar 15 09:47:37 2004

QY 92 AVYCAR 98
Db 84 AVYCAR 90

RESULT 15
Q9UC53 PRELIMINARY; PRT; 16 AA.
AC Q9UC53
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 77 kDa SPONTANEOUS RECURRENT ABORTION-associated human embryonic antigen/IGHIII homolog (Fragment).
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=96033130; PubMed=8582963;
RA Shiraishi Y., Shiraishi Y., Yamamoto D., Hasegawa T., Kitamura W.,
RA Miki S., Tanaka T., Suzuki T., Soma H.;
RT "Diagnostic relevance of abortion-associated human embryonic antigen
RT expressed on the cell surface of tumour promoter-treated Bloom syndrome
RL Hum. Reprod. 10:1694-1701(1995).
SQ SEQUENCE 16 AA; 1626 MW; C9C5ED2512FF3FB9 CRC64;

Query Match 5.2%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GLVQPG 15
Db 10 GLVQPG 15

RESULT 16
Q91HB1 PRELIMINARY; PRT; 29 AA.
AC Q91HB1
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Porcine circovirus type 2.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
OX NCBI_TaxID=85708;
RN [1]
RP SEQUENCE FROM N.A.
RA Shengbo C., Huanhun C.;
RT "Cloning and sequence analysis of the genome of Porcine Circovirus
RT type 2 isolated from pig with PMWS in China."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY035820; AAK60466.1; -.
KW Hypothetical protein.
SQ SEQUENCE 29 AA; 3223 MW; 87D7DC201205CEC7 CRC64;

Query Match 5.2%; Score 6; DB 12; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGSRL 20
Db 11 GGSRL 16

RESULT 17
O15224 PRELIMINARY; PRT; 38 AA.
ID O15224
AC O15224;

DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CDR3-IGM (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Follicle centre lymphoma;
RX MEDLINE=98261457; PubMed=9596578;
RA Ottensmeier C.H., Thompson A.R., Zhu D., Wilkins B.S.,
RA Sweteham J.W., Stevenson F.K.;
RT "Analysis of VH genes in follicular and diffuse lymphoma shows ongoing
RT somatic mutation and multiple isotype transcripts in early disease
RL Blood 91:4292-4299(1998).
DR EMBL; AJ001411; CAA04746.1; -.
DR HSP; P01810; 2PBJ.
DR InterPro; IPR007110; IG-like.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4365 MW; C68B5B68A32ECD5 CRC64;

Query Match 5.2%; Score 6; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 LVTSS 115
Db 22 LVTSS 27

RESULT 18
Q8WNG3 PRELIMINARY; PRT; 44 AA.
AC Q8WNG3
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NPIP-like protein (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LCR15a duplication region;
RX MEDLINE=21470411; PubMed=11586358;
RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,
RA Rocchi M., Eichler E.E.;
RT "Positive selection of a gene family during the emergence of humans
RT and African apes."
RL Nature 413:514-519(2001).
DR EMBL; AF364277; AAL50491.1; -.
FT NON_TER 1
FT NON_TER 44
SQ SEQUENCE 44 AA; 4985 MW; A875B2DA8DB7D3C3 CRC64;

Query Match 5.2%; Score 6; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGSRL 20
Db 16 GGSRL 21

RESULT 19
Q8EV56 PRELIMINARY; PRT; 58 AA.
ID Q8EV56
AC Q8EV56;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN MYEE7115.
 OS Mycoplasma penetrans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=28227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HF-2;
 RX MEDLINE=22354719; PubMed=12466555;
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
 RT "The complete genomic sequence of Mycoplasma penetrans, an
 RT intracellular bacterial pathogen in humans.";
 RL Nucleic Acids Res. 30:5293-5300(2002).
 DR EMBL; AP004173; BAC44504.1;
 DR EMBL; AP004173; BAC44504.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 58 AA; 6743 MW; 82751A7819556B18 CRC64;
 Query Match 5.2%; Score 6; DB 16; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 53 YDGSNK 58
 Db 41 YDGSNK 46
 RESULT 20
 ID OSQ063 PRELIMINARY; PRT; 66 AA.
 AC OSQ063;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Orthopoxvirus.
 DE CWP60.5L.
 DE CWP60.5L.
 GN CWP60.5L.
 OS Camelpox virus (strain CP-1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203174;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWS;
 RX PubMed=11907335;
 RA Gubser C., Smith G.L.;
 RT "The sequence of camelpox virus shows it is most closely related to
 RT variola virus, the cause of smallpox.";
 RL J. Gen. Virol. 83:855-872(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWS;
 RA Gubser C., Smith G.L.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY009089; AAG37525.1;
 SQ SEQUENCE 66 AA; 7633 MW; 0B9BBA120088110A CRC64;
 Query Match 5.2%; Score 6; DB 12; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 27 FTFSSY 32
 Db 38 FTFSSY 43
 RESULT 21
 ID OSQJFD1 PRELIMINARY; PRT; 66 AA.
 AC OSQJFD1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Vaccinia virus (strain Tian Tan).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OX NCBI_TaxID=10253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tian Tan;
 RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
 RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
 RT "Complete genomic sequence of vaccinia virus (Tian Tan strain).";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF095689; AAF33921.1;
 KW Hypothetical protein.
 SQ SEQUENCE 66 AA; 7618 MW; 0D460CCFB088110A CRC64;
 Query Match 5.2%; Score 6; DB 12; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 27 FTFSSY 32
 Db 38 FTFSSY 43
 RESULT 22
 ID OSQYN75 PRELIMINARY; PRT; 67 AA.
 AC OSQYN75;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Ribosomal protein S17.
 DE Eimeria tenella.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
 OC Eimeria.
 OX NCBI_TaxID=5802;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cai X., Zhu G.;
 RT "Eimeria tenella plastid genome complete sequence.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY217738; AAO40228.1;
 SQ Chloroplast; Ribosomal protein.
 SQ SEQUENCE 67 AA; 8291 MW; CECADFCF65621A6 CRC64;
 Query Match 5.2%; Score 6; DB 8; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 56 SNKYIA 61
 Db 11 SNKYIA 16
 RESULT 23
 ID OSQ8Q32 PRELIMINARY; PRT; 70 AA.
 AC OSQ8Q32;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Predicted protein.
 GN MA1720.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.

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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:29:28 ; Search time 17 Seconds
(without alignments)
352.239 Million cell updates/sec

Title: us-09-620-955b-2
Perfect score: 115
Sequence: 1 QVQLQESGGGLVQPGSRL.....CARDRYFDLWGRGLVTVSS 115

Scoring table: OLIGO
Gapo 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19291

Minimum DB seq length: 0
Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database : SwissProt-42

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	21.7	115	1 HV3D HUMAN	P01765 homo sapien
2	19	16.5	114	1 HV01 CANFA	P01784 canis faml
3	17	14.8	115	1 HV3S HUMAN	P01780 homo sapien
4	16	13.9	115	1 HV3F HUMAN	P01767 homo sapien
5	14	12.2	114	1 HV3B HUMAN	P01763 homo sapien
6	13	11.3	97	1 HV56 MOUSE	P18527 mus musculus
7	13	11.3	98	1 HV57 MOUSE	P18528 mus musculus
8	12	10.4	111	1 HV35 MOUSE	P01804 mus musculus
9	12	10.4	113	1 HV27 MOUSE	P01796 mus musculus
10	12	10.4	113	1 HV28 MOUSE	P01797 mus musculus
11	12	10.4	113	1 HV29 MOUSE	P01798 mus musculus
12	12	10.4	113	1 HV30 MOUSE	P01799 mus musculus
13	12	10.4	113	1 HV31 MOUSE	P01800 mus musculus
14	12	10.4	115	1 HV32 MOUSE	P01801 mus musculus
15	12	10.4	115	1 HV33 MOUSE	P01802 mus musculus
16	11	9.6	113	1 HV34 MOUSE	P01803 mus musculus
17	7	6.1	113	1 HV47 MOUSE	P01823 mus musculus
18	7	6.1	114	1 HV00 MOUSE	P01741 mus musculus
19	7	6.1	114	1 HV2A RABIT	P01827 oryctolagus
20	7	6.1	115	1 HV44 MOUSE	P01820 mus musculus
21	6	5.2	66	1 HVED VACCV	P20556 vaccinia vi
22	6	5.2	67	1 RPOZ BACSD	O35011 bacillus su
23	6	5.2	68	1 RPOZ BACHD	O9K9Y3 bacillus ha
24	6	5.2	93	1 NEUI STRCA	P15444 struthio ca
25	6	5.2	102	1 YG81 WOLSU	O34247 wolinnella s
26	6	5.2	106	1 YF81 ARCFU	O28691 archaeglob
27	6	5.2	107	1 Y231 RHIME	O92ax1 rhizobium m
28	6	5.2	107	1 YJ09 BRUME	O8yeg9 bruceella me
29	6	5.2	111	1 Y6G8 PSEPK	O88f31 pseudomonas
30	6	5.2	115	1 NU3M DUGDU	O8w9m9 dugong dugo
31	6	5.2	115	1 NU3M RABIT	O79434 oryctolagus
32	5	4.3	27	1 GRP CHICK	P01295 gallus gall
33	5	4.3	40	1 R36Z_STRCO	Q93jh3 streptomyce

ALIGNMENTS

RESULT 1

```
HV3D HUMAN
ID HV3D HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and Genetics. Identity between variable
regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
IDENTICAL.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02048; H3HUTL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 108 IG-LIKE.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 21.7%; Score 25; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.6e-19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ESGGGLVQGGSLRLSCAASGFTFS 30
DB 6 ESGGGLVQGGSLRLSCAASGFTFS 30

RESULT 2
HV01 CANFA
ID HV01 CANFA STANDARD; PRT; 114 AA.
AC P01784;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region GOW.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=77242369; PubMed=407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
immunoglobulin heavy chains.";
RL Biochemistry 16:3160-3168(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02067; AVDGM.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.

HV3F HUMAN
ID HV3F HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 112 IG-LIKE.
NON TER 115 115
SEQUENCE 115 AA; 12563 MW; 68B668E531C12514 CRC64;

Query Match 14.8%; Score 17; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 PGGSRLSLSCAASGFTFS 30
DB 14 PGGSRLSLSCAASGFTFS 30

RESULT 4
HV3F HUMAN
ID HV3F HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
IG2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02050; A2HUBU.
DR HSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 13.9%; Score 16; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QPGGSLRLSCAASGFT 28
DB 13 QPGGSLRLSCAASGFT 28
|||||

RESULT 5
HV3B_HUMAN STANDARD; PRT; 114 AA.
ID HV3B_HUMAN
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02046; M3HWE.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT NON_TER 114
SQ SEQUENCE 114 AA; 12256 MW; D86294FB418A07B7 CRC64;

Query Match 12.2%; Score 14; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISR 72
DB 59 YYADSVKGRFTISR 72
|||||

RESULT 6
HV56_MOUSE STANDARD; PRT; 97 AA.
ID HV56_MOUSE
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RA MEDLINE=89279149; PubMed=2499654;
RX Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; J10504; HVNS91.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 11.3%; Score 13; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LSCAASGFTFSY 32
DB 20 LSCAASGFTFSY 32
|||||

RESULT 7
HV57_MOUSE STANDARD; PRT; 98 AA.
ID HV57_MOUSE
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RA MEDLINE=89279149; PubMed=2499654;
RX Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during

```
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE HV7183 SUBFAMILY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; J0501; HVMS96.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 >98 IG-LIKE.
FT NON_TER 98
FT SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 11.3%; Score 13; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 DSVKGRFTISRDN 74
DB 62 DSVKGRFTISRDN 74
|||||

RESULT 8
HV35_MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HPC76 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions Genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02074; MHMS76.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1
FT NON_TER 111
FT DOMAIN <1 110 IG-LIKE.
FT SEQUENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;

Query Match 10.4%; Score 12; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 1 ESGGGLVQPGGS 12
|||||

RESULT 9
HV27_MOUSE STANDARD; PRT; 113 AA.
ID HV27_MOUSE
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17
|||||

RESULT 10
HV28_MOUSE STANDARD; PRT; 113 AA.
ID HV28_MOUSE
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
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FT NON TER 113
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 11
HV29 MOUSE
ID HV29 MOUSE STANDARD; PRT; 113 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc Natl Acad Sci U S A. 75:1957-1961(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C93818; AVMS57.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12647 MW; E50F2P20EDB129B CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 12
HV30 MOUSE
ID HV30 MOUSE STANDARD; PRT; 113 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
proteins.";
RL Biochemistry 16:1170-1175(1977).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 13
HV31 MOUSE
ID HV31 MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A92810; AVMS57.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 14
HV32 MOUSE
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ID HV32_MOUSE STANDARD; PRT; 115 AA.
AC P01801;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C92811; AVMS06.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; B67AD6638A121A5P CRC64;

Query Match 10.4%; Score 12; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
Db 6 ESGGGLVQPGGS 17

RESULT 15
HV33_MOUSE STANDARD; PRT; 115 AA.
ID HV33_MOUSE
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; D92811; AVMS82.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; B67AD6638A121A5P CRC64;

Query Match 10.4%; Score 12; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
Db 6 ESGGGLVQPGGS 17

RESULT 16
HV34_MOUSE STANDARD; PRT; 113 AA.
ID HV34_MOUSE
AC P01803;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region AMPC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
RT evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02073; HVMSAM.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 7A6D906AAA966E9E CRC64;

Query Match 9.6%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 SVKGRFTISR 73
Db 65 SVKGRFTISR 75

RESULT 17
HV47_MOUSE STANDARD; PRT; 113 AA.
ID HV47_MOUSE
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-60.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84024551; PubMed=6414509;
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 9B4517648C121C5A CRC64;

Query Match 10.4%; Score 12; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 9B4517648C121C5A CRC64;

Query Match 10.4%; Score 12; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
Db 6 ESGGGLVQPGGS 17

RESULT 16
HV34_MOUSE STANDARD; PRT; 113 AA.
ID HV34_MOUSE
AC P01803;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region AMPC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
RT evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02073; HVMSAM.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 7A6D906AAA966E9E CRC64;

Query Match 9.6%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 SVKGRFTISR 73
Db 65 SVKGRFTISR 75

RESULT 17
HV47_MOUSE STANDARD; PRT; 113 AA.
ID HV47_MOUSE
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-60.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84024551; PubMed=6414509;
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 9B4517648C121C5A CRC64;

Query Match 10.4%; Score 12; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RA Juszczak E.C., Margolles M.N.;
 RT "Amino acid sequence of the heavy chain variable region from the A/J
 RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
 RT idiotype."
 RL Biochemistry 22:4291-4296(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
 CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
 CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
 CC STRAIN A/J MICE.
 CC PIR; A02098; G2MS60.
 DR PDB; 1J10; 18-FEB-03.
 DR PDB; 1J1P; 18-FEB-03.
 DR PDB; 1J1X; 18-FEB-03.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; 3D-structure.
 FT NON TER 113 114
 SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0B3F5075B7 CRC64;
 Query Match 6.1%; Score 7; DB 1; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VOLQESG 8
 DB 2 VOLQESG 8
 RESULT 18
 HV00 MOUSE
 ID HV00 MOUSE STANDARD; PRT; 114 AA.
 AC P01741;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region (Anti-arsenate antibody).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=79195438; PubMed=109536;
 RA Capra J.D.; Nisonoff A.;
 RT "Structural studies on induced antibodies with defined idiotypic
 RT specificities. VII. The complete amino acid sequence of the heavy
 RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
 RT mice bearing a cross-reactive idiotype."
 RL J. Immunol. 123:279-284(1979).
 CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
 CC REGION SEQUENCE.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02022; G1MSAA.
 DR HSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 106
 FT NON TER 114 114
 SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A59F4BE CRC64;
 Query Match 6.1%; Score 7; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPG 42
 DB 36 WVRQAPG 42
 RESULT 19
 HV2A RABIT
 ID HV2A RABIT STANDARD; PRT; 114 AA.
 AC P01827;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-A2 region BS-1.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277871; PubMed=9073;
 RA Jaton J.-C.;
 RT "The V-region sequence of the H chain from a third rabbit anti-
 RT pneumococcal antibody."
 RL Biochem. J. 157:449-459(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
 CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02103; GARB21.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Pyrrrolidone carboxylic acid.
 FT DOMAIN 1 107
 FT MOD RES 1 1
 FT NON TER 114 114
 SQ SEQUENCE 114 AA; 12325 MW; 466F5EE1E55C1F96 CRC64;
 Query Match 6.1%; Score 7; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 WVRQAPG 42
 DB 36 WVRQAPG 41
 RESULT 20
 HV44 MOUSE
 ID HV44 MOUSE STANDARD; PRT; 115 AA.
 AC P01820;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region PUL4 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=6774258;
 RX MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 RT of complete immunoglobulin heavy-chain genes."
 RL Nature 286:676-683(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC EMBL; V00767; CRA24148.1; -;
 CC PIR; A02095; HVMG14.
 CC PDB; 1A7N; 29-APR-98.
 CC PDB; 1A7O; 29-APR-98.
 CC PDB; 1A7P; 29-APR-98.
 CC PDB; 1A7R; 29-APR-98.
 CC PDB; 1G7H; 17-JAN-01.
 CC PDB; 1G7I; 17-JAN-01.
 CC PDB; 1G7J; 17-JAN-01.
 CC PDB; 1G7M; 17-JAN-01.
 CC PDB; 43C9; 24-JUL-02.
 CC PDB; 43CA; 24-JUL-02.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00405; IGV; 1.
 CC PROSITE; PS0835; IG LIKE; 1.
 CC Immunoglobulin V region; Signal; 3D-structure.
 CC SIGNAL 19
 CC CHAIN 20 115 IG HEAVY CHAIN V REGION PJ14.
 CC DOMAIN 20 >115 IG-LIKE.
 CC NON_TER 115 115
 CC SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

Query Match 6.1%; Score 7; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PKGLEW 47
 DB 60 PKGLEW 66

RESULT 21
 ID YVED_VACC STANDARD; PRT; 66 AA.
 AC P20556;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 7.6 kDa protein.
 GN E ORF D.
 OS Vaccinia virus (strain Copenhagen).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OC NCBI_TaxID=10249;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "The complete DNA sequence of vaccinia virus."
 RL Virology 179:247-266(1990).
 RN [2]
 RP COMPLETE GENOME.
 RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "Appendix to 'The complete DNA sequence of vaccinia virus'";
 RL Virology 179:517-563(1990).

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DR EMBL; M35027; AAA48048.1; -;
 DR PIR; A42510; A42510.
 DR KW Hypothetical protein.
 DR SEQUENCE 66 AA; 7645 MW; 0D57ED3FB0880C17 CRC64;

Query Match 5.2%; Score 6; DB 1; Length 66;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 FTFSSY 32
 DB 38 FTFSSY 43

RESULT 22

RPOZ_BACSU STANDARD; PRT; 67 AA.

AC Q35011;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable DNA-directed RNA polymerase omega chain (EC 2.7.7.6)
 DE (Transcriptase omega chain) (RNA polymerase omega subunit).
 GN RPOZ OR BSU15690.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=168;
 RC MEDLINE=98195738; PubMed=9534248;
 RA Foulger D., Errington J.;
 RT "A 28 kbp segment from the spoVM region of the Bacillus subtilis 168
 genome".
 RL Microbiology 144:801-805(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Betero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codan J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entiaz K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallaron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppe H., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescecian E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche M., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sato T., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Srokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,
 RA Tsutao V., Uchiyama S., Vandenbol M., Vanlier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzreger T.,
 RA Winters P., Wipatt A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis".
 RL Nature 390:249-256(1997).

CC -!- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-
 CC terminal regions of the beta' subunit thereby facilitating its
 CC interaction with the beta and alpha subunits (By similarity).

CC -|- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA] (N).
CC -|- SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which
CC is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1
CC omega chain (By similarity).
CC
CC -|- SIMILARITY: Belongs to the RNA polymerase omega chain family.
CC
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CC
CC EMBL: Y13937; CA474272.1; -
CC EMBL: Z99112; CAB13442.1; -
CC PIR: C69878; C69878.
CC HAMAP: MF_00366; -; 1.
CC InterPro: IPR003716; RNA_pol_omega.
CC InterPro: IPR006110; RNA_pol_Rpb6.
CC Pfam: PF01192; RNA_pol_Rpb6; 1.
CC TIGRFAMs: TIGR00690; rpoZ; 1.
CC Transferrase; DNA-directed RNA polymerase; Transcription;
CC Complete proteome.
CC
CC Query Match 5.2%; Score 6; DB 1; Length 67;
CC Best Local Similarity 100.0%; Pred. No. 32;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 109 TLTVTS 114
CC Db |||||
CC 18 TLTVTS 23
CC
CC RESULT 23
CC RPOZ BACHD STANDARD; PRT; 68 AA.
CC ID RPOZ BACHD
CC AC Q9K9Y3;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Probable DNA-directed RNA polymerase omega chain (EC 2.7.7.6)
CC DE (Transcriptase omega chain) (RNA polymerase omega subunit).
CC GN RPOZ OR BH2511.
CC OS Bacillus halodurans.
CC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC OX NCBI_TaxID=86665;
CC RN [1]
CC SEQUENCE FROM N.A.
CC RC STRAIN=C-125 / JCM 9153;
CC RX MEDLINE=20512582; PubMed=11058132;
CC RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Maui N.,
CC Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
CC Horikoshi K.
CC RA "Complete genome sequence of the alkaliphilic bacterium Bacillus
CC halodurans and genomic sequence comparison with Bacillus subtilis."
CC Nucleic Acids Res. 28:4317-4331(2000).
CC -|- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-
CC terminal regions of the beta' subunit thereby facilitating its
CC interaction with the beta and alpha subunits (By similarity).
CC -|- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA] (N).
CC -|- SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which
CC is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1
CC omega chain (By similarity).
CC -|- SIMILARITY: Belongs to the RNA polymerase omega chain family.
CC
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CC
CC EMBL: AP001515; BAB06230.1; -
CC PIR: G83963; G83963.
CC HAMAP: MF_00366; -; 1.
CC InterPro: IPR003716; RNA_pol_omega.
CC InterPro: IPR006110; RNA_pol_Rpb6.
CC Pfam: PF01192; RNA_pol_Rpb6; 1.
CC TIGRFAMs: TIGR00690; rpoZ; 1.
CC Transferrase; DNA-directed RNA polymerase; Transcription;
CC Complete proteome.
CC
CC Query Match 5.2%; Score 6; DB 1; Length 68;
CC Best Local Similarity 100.0%; Pred. No. 32;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 109 TLTVTS 114
CC Db |||||
CC 18 TLTVTS 23
CC
CC RESULT 24
CC NEUL STRCA STANDARD; PRT; 93 AA.
CC ID NEUL STRCA
CC AC P15444;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Neurophysin 1.
CC OS Struthio camelus (Ostrich).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
CC OC Struthio.
CC OX NCBI_TaxID=8801;
CC RN [1]
CC SEQUENCE.
CC RX MEDLINE=88138569; PubMed=3436699;
CC RA Lazure C., Saayman H.S., Naude R.J., Oelofsen W., Chretien M.,
CC "Complete amino acid sequence of a VLDV-type neurophysin from ostrich
CC differs markedly from known mammalian neurophysins."
CC Int. J. Pept. Protein Res. 30:634-645(1987).
CC -|- FUNCTION: NEUROPHYSIN 1 SPECIFICALLY BINDS OXYTOCIN.
CC -|- SIMILARITY: Belongs to the vasopressin/oxytocin family.
CC PIR: J50301; J50301.
CC DR HSSP; P01180; 2BN2.
CC DR InterPro: IPR000981; Neurhyp_horm.
CC DR Pfam: PF00184; hormones; 1.
CC DR PRINTS: PR00831; NEUROPHYSIN.
CC DR ProDom: PD001676; Neurhyp_horm; 1.
CC DR SMART; SM00003; NH; 1.
CC FT DISULFID 10 54 BY SIMILARITY.
CC FT DISULFID 13 27 BY SIMILARITY.
CC FT DISULFID 28 34 BY SIMILARITY.
CC FT DISULFID 21 44 BY SIMILARITY.
CC FT DISULFID 61 74 BY SIMILARITY.
CC FT DISULFID 68 86 BY SIMILARITY.
CC FT DISULFID 75 80 BY SIMILARITY.
CC SQ SEQUENCE 93 AA; 9971 MW; 7C8A9FBE2AC1444 CRC64;
CC
CC Query Match 5.2%; Score 6; DB 1; Length 93;
CC Best Local Similarity 100.0%; Pred. No. 43;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 21 SCAASG 26
CC Db |||||
CC 67 SCAASG 72
CC
CC RESULT 25

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Job time : 21 secs